SEQUENCE LISTING

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Alfredo Nicosio
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Annalisa Meola

<120> CHIMPANZEE ADENOVIRUS VACCINE CARRIERS

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<150> PCT/EP2005/000558
<151> 2004-01-18

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<211> 1278
<212> DNA
<213> Chimpanzee Adenovirus- ChAd 4 Fiber

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<211> 1335
<212> DNA
<213> Chimpanzee Adenovirus- ChAd 5 Fiber

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<210> 9
<211> 1338
<212> DNA
<213> Chimpanzee Adenovirus- ChAd 7 Fiber

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<210> 10
<211> 1278
<212> DNA
<213> Chimpanzee Adenovirus- ChAd 9 Fiber

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acctggacta atggaagcta tgttggagca acatttggag ctaactctta taccttctcc 1260
tacatcgccc aagaatga 1278

<210> 11
<211> 1278
<212> DNA
<213> Chimpanzee Adenovirus- ChAd 10 Fiber

<400> 11
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gagaagcccc tgggggtgct gtccctgcga ctggccgacc ccgtcaccac caagaacggg 180
gaaatcaccc tcaagctggg agagggggtg gacctcgact cctcgggaaa actcatctcc 240
aacacggcca ccaaggccgc cgcccctctc agtttttcca acaacaccat ttcccttaac 300
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aatatactga gaacaagcat tctaaacaca ctagctttag gttttggatc aggtttagga 420
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aacataagct gggctaaagg tttaaaattt gaagatggag ccatagcaac caacattgga 600
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tacatcgccc aagaatga 1278

<210> 12
<211> 1737
<212> DNA
<213> Chimpanzee Adenovirus- ChAd 11 Fiber

<400> 12
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acctcagccc ccctgactgt gagcacctca ggcgccctca ccctagcagc cgccgttccc 360
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attaatgaaa cgttccaaac caactctttc accttctcct acatcgccca agaataa 1737

<210> 13
<211> 1632
<212> DNA
<213> Chimpanzee Adnovirus- ChAd 16 Fiber

<400> 13
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aacggtcctc cctccgtccc tttcctcacc cctcccttcg tgtctcccga tggattccaa 120
gagagccccc ccggggtcct gtctctgaac ctggccgagc ccctggtcac ttcccacggc 180
atgctcgccc tgaaaatggg aagtggcctc tccctggacg acgccggcaa cctcacctct 240
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acctcagccc ccctgactgt gagcacctca ggcgccctca ccctagcagc cgccgccccc 360
ctggcggtgg ccggcacctc cctcaccatg caatcagagg ccccccctgac agtccaagat 420
gcaaaactca ccctggccac caagggcccc ctgaccgtgt ctgaaggcaa actggccttg 480
cagacctcgg ccccgctgac ggccgctgac agcagcaccc tcaccgttag cgccacacca 540
cccatcagtg taagcagtgg aagtttgggc ttagacatgg aagacccaat gtatactcat 600
gatggaaaac tgggaataag aattgggggc ccactgagag tagtagacag cctgcacaca 660
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gtttacttga atggggacaa atccaaaccc atgaccctta ccattaccct caatggaact 1500
aatgaatcca gtgaaactag ccaggtgagt cactactcca tgtcatttac gtgggcttgg 1560
gagagtgggc aatatgccac cgaaaccttt gccaccaatt cctttacctt ctcttacatt 1620
gctgaacaat aa 1632

<210> 14
<211> 1632
<212> DNA
<213> Chimpanzee Adenovirus-ChAd 17 Fiber

<400> 14
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gaaagccccc ccggggtcct gtctctgaac ctggccgagc ccctggtcac ttcccacggc 180
atgcttgccc tgaaaatggg aagtggcctc tccctggacg acgctggcaa ccttacctct 240
caagatatta cctccactac ccctcccctc aaaaaaacca agaccaacct cagcctagaa 300
acctcatccc ccctaactgt aagcacctca ggcgccctca ccgtagcagc cgccgctccc 360
ctggcggtgg ccggcacctc cctcaccatg caatcagagg ccccccctggc agtacaggat 420
gcaaaactca ccctggccac caaaggcccc ctgaccgtgt ctgaaggcaa actggccttg 480
caaacatcgg ccccgctgac ggccgctgac agcagcaccc tcaccgttag ctccactcca 540
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gatggaaaac tgggaataag aattgggggt ccactaagag tagtagacag cttgcacaca 660
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aatgaatcca gtgaaactag tcaggtgagt cactactcca tgtcatttac atgggcttgg 1560
gaaagcgggc aatatgccac tgaaaccttt gccaccaact ccttcacctt ttcttacatt 1620
gctgaacaat aa 1632

<210> 15
<211> 1632
<212> DNA
<213> Chimpanzee Adenovirus- ChAd 19 Fiber

<400> 15
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aacggtcctc cctccgtccc tttcctcacc cctcccttcg tgtctcccga tggattccaa 120
gagagccccc ccggggtcct gtctctgaac ctggccgagc ccctggtcac ttcccacggc 180
atgctcgccc tgaaaatggg aagtggcctc tccctggacg acgccggcaa cctcacctct 240
caagatgtca ccaccactac ccctcccctg aaaaaaacca agaccaacct cagcctagaa 300

acctcagccc ccctgactgt gagcacctca ggcgccctca ccctagcagc cgccgccccc 360
ctggcggtgg ccggcacctc cctcaccatg caatcagagg ccccccctgac agtccaagat 420
gcaaaactca ccctggccac caagggcccc ctgaccgtgt ctgaaggcaa actggccttg 480
cagacctcgg ccccgctgac ggccgctgac agcagcaccc tcaccgttag cgccacacca 540
cccatcagtg taagcagtgg aagtttgggc ttagacatgg aagacccaat gtatactcat 600
gatggaaaac tgggaataag aattgggggc ccactgagag tagtagacag cctgcacaca 660
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gtttacttga atggggacaa atccaaaccc atgaccctta ccattaccct caatggaact 1500
aatgaatcca gtgaaactag ccaggtgagt cactactcca tgtcatttac gtgggcttgg 1560
gagagtgggc aatatgccac cgaaaccttt gccaccaatt cctttacctt ctcttacatt 1620
gctgaacaat aa 1632

<210> 16
<211> 2865
<212> DNA
<213> Chimp0anzee Adenovirus- ChAd 20 Hexon

<400> 16
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ctgagtaaca agtttaggaa ccccacggtg gcgcccacgc acgatgtgac caccgaccgg 180
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tacaactccc tggcccccaa gggcgctccc aacccatgcg agtgggatga ggctgctact 420
gcccttgaca ttgatttgaa cgcagaagac gatgaagaaa gcgacgaagc tcaaggggaa 480
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ctgttcgaag tctttgacgt ggtccgggtc caccagccgc accgcggcgt catcgagacc 2820
gtgtacctgc gtacgccctt ctcggccggc aacgccacca cctaa 2865

<210> 17
<211> 2823
<212> DNA
<213> Chimpanzee Adenovirus- ChAd 4 Hexon

<400> 17
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<211> 2823
<212> DNA
<213> Chimpanzee Adenovirus- ChAd 5 Hexon

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<210> 19
<211> 2823
<212> DNA
<213> Chimpanzee Adenovirus- ChAd 7 Hexon

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<211> 2793
<212> DNA
<213> Chimpanzee Adenovirus- ChAd 9 Hexon

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<210> 21
<211> 2793
<212> DNA
<213> Chimpanzee Adenovirus- ChAd 10 Hexon

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<211> 2883
<212> DNA
<213> Chimpanzee Adenovirus- ChAd 11 Hexon

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taa 2883

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<211> 2835
<212> DNA
<213> Chimpanzee Adenovirus- ChAd 16 Hexon

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<211> 2883
<212> DNA
<213> Chimpanzee Adenovirus- ChAd 17 Hexon

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taa 2883

<210> 25
<211> 2877
<212> DNA
<213> Chimpanzee Adenovirus- ChAd 19 Hexon

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<220>
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<210> 27
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<210> 28
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<220>
<223> Oligomer

<400> 28

cgctggcact caagagtggc ctc 23

<210> 29
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<400> 29
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<210> 30
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<220>
<223> Oligomer

<400> 30
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<210> 31
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<223> Oligomer

<400> 31
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<210> 32
<211> 33
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<213> Artificial Sequence

<220>
<223> Oligomer

<400> 32
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<210> 41
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<213> Chimpanzee Adenovirus- ChAd 3 Hexon

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ctctacccca tacccgccaa cgccaccaac gtccccatct ccatcccctc gcgcaactgg 2040
gcggccttcc gcggctgggc cttcacccgc ctcaagacca aggagacccc ctccctgggc 2100
tcgggattcg acccctacta cacctactcg ggctctattc cctacctgga cggcaccttc 2160
tacctcaacc acactttcaa gaaggtctcg gtcaccttcg actcctcggt cagctggccg 2220
ggcaacgacc gtctgctcac ccccaacgag ttcgagatca agcgctcggt cgacggggaa 2280
ggctacaacg tggcccagtg caacatgacc aaggactggt tcctggtcca gatgctggcc 2340
aactacaaca tcggctacca gggcttctac atcccagaga gctacaagga caggatgtac 2400
tccttcttca ggaacttcca gcccatgagc cggcaggtgg tggaccagac caagtacaag 2460
gactaccagg aggtgggcat catccaccag cacaacaact cgggcttcgt gggctacctc 2520
gcccccacca tgcgcgaggg acaggcctac cccgccaact tcccctaccc gctcataggc 2580
aagaccgcgg tcgacagcat cacccagaaa aagttcctct gcgaccgcac cctctggcgc 2640
atccccttct ccagcaactt catgtccatg ggtgcgctct cggacctggg ccagaacttg 2700
ctctacgcca actccgccca cgccctcgac atgaccttcg aggtcgaccc catggacgag 2760
cccacccttc tctatgttct gttcgaagtc tttgacgtgg tccgggtcca ccagccgcac 2820
cgcggcgtca tcgagaccgt gtacctgcgt acgcccttct cggccggcaa cgccaccacc 2880

<210> 42
<211> 1683
<212> DNA
<213> Chimpanzee Adenovirus- ChAd 3 Fiber

<400> 42
atgtcagatt cttgctcctg tccctccgca cccactatct tcatgttgtt gcagatgaag 60
cgcaccaaaa cgtctgacga gagcttcaac cccgtgtacc cctatgacac ggaaagcggc 120
cctccctccg tccctttcct caccctctcc ttcgtgtctc ccgatggatt ccaagaaagc 180
ccccccgggg tcctgtctct gaacctggcc gagcccctgg tcacttccca cggcatgctc 240
gccctgaaaa tgggaagtgg cctctccctg gacgacgctg gcaacctcac ctctcaagat 300
atcaccaccg ctagccctcc cctcaaaaaa accaagacca acctcagcct agaaacctca 360
tccccctaa ctgtaagcac ctcaggcgcc ctcaccgtag cagccgccgc tcccctggca 420
gtggccggca cctccctcac catgcaatca gaggcccccc tgacagtaca ggatgcaaaa 480
ctcaccctgg ccaccaaagg ccccctgacc gtgtctgaag gcaaactggc cttgcaaaca 540
tcggccccgc tgacggccgc tgacagcagc accctcaccg ttagcgccac accaccaatt 600
aatgtaagca gtggaagttt aggcttagac atggaagacc ctatgtatac tcacgatgga 660
aaactgggaa taagaattgg gggtccacta agagtagtag acagcttgca cacactcact 720
gtagttaccg gaaatggact aactgtagat aacaatgccc tccaaactag agttacgggc 780
gccctaggtt atgacacatc aggaaatcta caattgagag ctgcaggagg tatgcgaatt 840
gatgcaaatg gccaacttat ccttaatgtg gcatacccat ttgatgctca gaacaatctc 900
agccttagac ttggtcaggg acccctgtat ataaacacag accacaacct ggatttgaat 960
tgcaacagag gtctaaccac aactaccacc aacaacacaa aaaaacttga gactaaaatt 1020
agctcaggct tagactatga caccaatggt gctgtcatta ttaaacttgg cactggtcta 1080
agcttcgaca acacaggcgc cctaactgtg ggaaacactg gtgatgataa actgactctg 1140
tggacgaccc cagacccatc tccaaattgc agaattcact cagacaaaga ctgcaagttt 1200
actctagtcc taactaagtg tggaagccaa atcctggcct ctgtcgccgc cctagcggta 1260
tcaggaaatc tggcttcgat aacaggcacc gttgccagcg ttaccatctt tctcagattt 1320
gatcagaatg gagtgcttat ggaaaactcc tcgctagaca ggcagtactg gaacttcaga 1380
aatggcaact caactaacgc tgccccctac accaatgcag ttgggttcat gccaaacctc 1440

gcagcatacc ccaaaacgca aagccagact gctaaaaaca acattgtaag tcaggtttac 1500
ttgaatggag acaaatccaa acccatgacc cttaccatca ccctcaatgg aactaatgaa 1560
tccagtgaaa ctagccaggt gagtcactac tccatgtcat ttacatgggc ttgggaaagt 1620
gggcaatatg ccactgaaac ctttgccacc aactccttca ccttttctta cattgctgaa 1680
caa 1683

<210> 43
<211> 2859
<212> DNA
<213> Chimpanzee Adenovirus- ChAd 6 Hexon

<400> 43
atgtatgtcc gccgaccaga aggaagaggc gcgtcgccga gttgcaagat ggccacccca 60
tcgatgctgc cccagtgggc gtacatgcac atcgccggac aggacgcttc ggagtacctg 120
agtccgggtc tggtgcagtt cgcccgcgcc acagacacct acttcagtct ggggaacaag 180
tttaggaacc ccacggtggc gcccacgcac gatgtgacca ccgaccgcag ccagcggctg 240
acgctgcgct tcgtgcccgt ggaccgcgag gacaacacct actcgtacaa agtgcgctac 300
acgctggccg tgggcgacaa ccgcgtgctg gacatggcca gcacctactt tgacatccgc 360
ggcgtgctgg atcggggccc cagcttcaaa ccctactccg gcaccgccta caacagcctg 420
gctcccaagg gagcgcccaa cacctcacag tggataacca aagacaatgg aactgataag 480
acatacagtt ttggaaatgc tccagtcaga ggattggaca ttacagaaga gggtctccaa 540
ataggacccg atgagtcagg gggtgaaagc aagaaaattt ttgcagacaa aacctatcag 600
cctgaacctc agcttggaga tgaggaatgg catgatacta ttggagctga agacaagtat 660
ggaggcagag cgcttaaacc tgccaccaac atgaaaccct gctatgggtc tttcgccaag 720
ccaactaatg ctaagggagg tcaggctaaa agcagaacca aggacgatgg cactactgag 780
cctgatattg acatggcctt ctttgacgat cgcagtcagc aagctagttt cagtccagaa 840
cttgttttgt atactgagaa tgtcgatctg gacaccccgg atacccacat tatttacaaa 900
cctggcactg atgaaacaag ttcttctttc aacttgggtc agcagtccat gcccaacaga 960
cccaactaca tcggcttcag agacaacttt atcggtctca tgtactacaa cagtactggc 1020
aatatgggtg tactagctgg acaggcctcc cagctgaatg ctgtggtgga cttgcaggac 1080
agaaacactg aactgtccta ccagctcttg cttgactctc tgggtgacag aaccaggtat 1140
ttcagtatgt ggaaccaggc ggtggacagc tacgaccccg atgtgcgcat tattgaaaat 1200
cacggtgtgg aggatgaact acccaactat tgcttccctt tgaatggtgt gggctttaca 1260
gatacattcc agggaattaa ggttaaaact accaataacg gaacagcaaa tgctacagag 1320
tgggaatctg atacctctgt caataatgct aatgagattg ccaagggcaa tcctttcgcc 1380
atggagatca acatccaggc caacctgtgg cggaacttcc tctacgcgaa cgtggcgctg 1440
tacctgcccg actcctacaa gtacacgccg gccaacatca cgctgcccgc caacaccaac 1500
acctacgatt acatgaacgg ccgcgtggta gcgccctcgc tggtggacgc ctacatcaac 1560
atcggggcgc gctggtcgct ggaccccatg gacaacgtca acccccttcaa ccaccaccgc 1620
aacgcgggcc tgcgctaccg ctccatgctc ctgggcaacg ggcgctacgt gcccttccac 1680
atccaggtgc cccaaaagtt tttcgccatc aagagcctcc tgctcctgcc cgggtcctac 1740
acctacgagt ggaacttccg caaggacgtc aacatgatcc tgcagagctc cctcggcaac 1800
gacctgcgca cggacggggc ctccatcgcc ttcaccagca tcaacctcta cgccaccttc 1860
ttccccatgg cgcacaacac cgcctccacg ctcgaggcca tgctgcgcaa cgacaccaac 1920
gaccagtcct tcaacgacta cctctcggcg gccaacatgc tctaccccat cccggccaac 1980
gccaccaacg tgcccatctc catcccctcg cgcaactggg ccgccttccg cggctggtcc 2040
ttcacgcgcc tcaagacccg cgagacgccc tcgctcggct ccgggttcga cccctacttc 2100
gtctactcgg gctccatccc ctacctcgac ggcaccttct acctcaacca caccttcaag 2160
aaggtctcca tcaccttcga ctcctccgtc agctggcccg gcaacgaccg cctcctgacg 2220
cccaacgagt tcgaaatcaa gcgcaccgtc gacggagagg ggtacaacgt ggcccagtgc 2280
aacatgacca aggactggtt cctggttcag atgctggccc actacaacat cggctaccag 2340
ggcttctacg tgcccgaggg ctacaaggac cgcatgtact ccttcttccg caacttccag 2400
cccatgagcc gccaggtcgt ggacgaggtc aactacaagg actaccaggc cgtcaccctg 2460
gcctaccagc acaacaactc gggcttcgtc ggctacctcg cgcccaccat gcgccaggga 2520
cagccctacc ccgccaacta cccctacccg ctcatcggca agagcgccgt cgccagcgtc 2580

acccagaaaa agttcctctg cgaccgggtc atgtggcgca tccccttctc cagcaacttc 2640
atgtccatgg gcgcgctcac cgacctcggc cagaacatgc tctacgccaa ctccgcccac 2700
gcgctagaca tgaatttcga agtcgacccc atggatgagt ccacccttct ctatgttgtc 2760
ttcgaagtct tcgacgtcgt ccgagtgcac cagccccacc gcggcgtcat cgaggccgtc 2820
tacctgcgca cgcccttctc ggccggtaac gccaccacc 2859

<210> 44
<211> 1335
<212> DNA
<213> Chimpanzee Adenovirus- ChAd 6 Fiber

<400> 44
atgtccaaaa agcgcgcgcg ggtggatgat gacttcgacc ccgtgtaccc ctacgatgca 60
gacaacgcac cgactgtgcc cttcatcaac cctcccttcg tctcttcaga tggattccaa 120
gaaaagcccc tgggggtgtt gtccctgcga ctggccgatc ccgtcaccac caagaacggg 180
gctgtcaccc tcaagctggg ggaggggggtg gacctcgacg actcgggaaa actcatctcc 240
aaaaatgcca ccaaggccac tgcccctctc agtatttcca acaacaccat ttcccttaac 300
atggataccc ctctttacaa caacaatgga aagctaggta tgaaggtaac cgcaccatta 360
aagatattag acacagatct actaaaaaca cttgttgttg cttatgggca gggattagga 420
acaaacacca atggtgctct tgttgcccaa ctagcatacc cacttgtttt taataccgct 480
agcaaaattg cccttaattt aggcaatgga ccattaaaag tggatgcaaa tagactgaac 540
attaattgca aaagaggtat ctatgtcact accacaaaag atgcactgga gattaatatc 600
agttgggcaa atgctatgac atttatagga aatgccattg gtgtcaatat tgacacaaaa 660
aaaggcctac agttcggcac ttcaagcact gaaacagatg ttaaaaatgc ttttccactc 720
caagtaaaac ttggagctgg tcttacattt gacagcacag gtgccattgt tgcttggaac 780
aaagaagatg acaaacttac actgtggacc acagccgatc catctccaaa ctgtcacata 840
tattctgcaa aggatgctaa gcttacactc tgcttgacaa agtgtggtag tcagatactg 900
ggcactgttt ctctcatagc tgttgatact ggtagcttaa atccaataac aggaaaagta 960
accactgctc ttgtttcact taaattcgat gccaatggag ttttgcaagc cagttcaaca 1020
ctagataaag aatattggaa tttcagaaaa ggagatgtga cacctgctga cccctacact 1080
aatgctatag gctttatgcc caaccttaat gcatacccaa aaaacacaaa cgcagctgca 1140
aaaagtcaca ttgttggaaa agtataccta catggggatg aaagcaagcc actagacttg 1200
ataattacat ttaatgaaac cagtgatgaa tcctgtactt attgcattaa ctttcagtgg 1260
cagtggggaa ctgaccaata taaagatgaa acacttgcag tcagttcatt caccttctca 1320
tacattgcta aagaa 1335

<210> 45
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 45
tgtcctacca rctcttgctt ga 22

<210> 46
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 46
gtggaarggc acgtagcg 18

<210> 47
<211> 9
<212> PRT
<213> HIV gag CD8 Epitope

<220>
<223> Primer

<400> 47
Ala Met Gln Met Leu Lys Glu Thr Ile
1 5

<210> 48
<211> 578
<212> PRT
<213> Chimpanzee Adenovirus- ChAd 20 Fiber

<400> 48
Met Lys Arg Thr Lys Thr Ser Asp Glu Ser Phe Asn Pro Val Tyr Pro
1 5 10 15
Tyr Asp Thr Glu Ser Gly Pro Pro Ser Val Pro Phe Leu Thr Pro Pro
20 25 30
Phe Val Ser Pro Asp Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser
35 40 45
Leu Asn Leu Ala Glu Pro Leu Val Thr Ser His Gly Met Leu Ala Leu
50 55 60
Lys Met Gly Ser Gly Leu Ser Leu Asp Asp Ala Gly Asn Leu Thr Ser
65 70 75 80
Gln Asp Ile Thr Thr Ala Ser Pro Pro Leu Lys Lys Thr Lys Thr Asn
85 90 95
Leu Ser Leu Glu Thr Ser Ser Pro Leu Thr Val Ser Thr Ser Gly Ala
100 105 110
Leu Thr Val Ala Ala Ala Ala Pro Leu Ala Val Ala Gly Thr Ser Leu
115 120 125
Thr Met Gln Ser Glu Ala Pro Leu Thr Val Gln Asp Ala Lys Leu Thr
130 135 140
Leu Ala Thr Lys Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu
145 150 155 160
Gln Thr Ser Ala Pro Leu Thr Ala Ala Asp Ser Ser Thr Leu Thr Val
165 170 175
Ser Ala Thr Pro Pro Leu Ser Thr Ser Asn Gly Ser Leu Gly Ile Asp
180 185 190
Met Gln Ala Pro Ile Tyr Thr Thr Asn Gly Lys Leu Gly Leu Asn Phe
195 200 205
Gly Ala Pro Leu His Val Val Asp Ser Leu Asn Ala Leu Thr Val Val
210 215 220
Thr Gly Gln Gly Leu Thr Ile Asn Gly Thr Ala Leu Gln Thr Arg Val
225 230 235 240
Ser Gly Ala Leu Asn Tyr Asp Thr Ser Gly Asn Leu Glu Leu Arg Ala
245 250 255
Ala Gly Gly Met Arg Val Asp Ala Asn Gly Gln Leu Ile Leu Asp Val

```
            260                 265                 270
Ala Tyr Pro Phe Asp Ala Gln Asn Asn Leu Ser Leu Arg Leu Gly Gln
        275                 280                 285
Gly Pro Leu Phe Val Asn Ser Ala His Asn Leu Asp Val Asn Tyr Asn
    290                 295                 300
Arg Gly Leu Tyr Leu Phe Thr Ser Gly Asn Thr Lys Lys Leu Glu Val
305                 310                 315                 320
Asn Ile Lys Thr Ala Lys Gly Leu Ile Tyr Asp Asp Thr Ala Ile Ala
                325                 330                 335
Ile Asn Ala Gly Asp Gly Leu Gln Phe Asp Ser Gly Ser Asp Thr Asn
            340                 345                 350
Pro Leu Lys Thr Lys Leu Gly Leu Gly Leu Asp Tyr Asp Ser Ser Arg
        355                 360                 365
Ala Ile Ile Ala Lys Leu Gly Thr Gly Leu Ser Phe Asp Asn Thr Gly
    370                 375                 380
Ala Ile Thr Val Gly Asn Lys Asn Asp Asp Lys Leu Thr Leu Trp Thr
385                 390                 395                 400
Thr Pro Asp Pro Ser Pro Asn Cys Arg Ile Tyr Ser Glu Lys Asp Ala
                405                 410                 415
Lys Phe Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Val Leu Ala Ser
            420                 425                 430
Val Ser Val Leu Ser Val Lys Gly Ser Leu Ala Pro Ile Ser Gly Thr
        435                 440                 445
Val Thr Ser Ala Gln Ile Val Leu Arg Phe Asp Glu Asn Gly Val Leu
    450                 455                 460
Leu Ser Asn Ser Ser Leu Asp Pro Gln Tyr Trp Asn Tyr Arg Lys Gly
465                 470                 475                 480
Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly Phe Met Pro
                485                 490                 495
Asn Leu Thr Ala Tyr Pro Lys Thr Gln Ser Gln Thr Ala Lys Ser Asn
            500                 505                 510
Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Ser Lys Pro Met Thr
        515                 520                 525
Leu Thr Ile Thr Leu Asn Gly Thr Asn Glu Thr Gly Asp Ala Thr Val
    530                 535                 540
Ser Thr Tyr Ser Met Ser Phe Ser Trp Asn Trp Asn Gly Ser Asn Tyr
545                 550                 555                 560
Ile Asn Glu Thr Phe Gln Thr Asn Ser Phe Thr Phe Ser Tyr Ile Ala
                565                 570                 575
Gln Glu
```

<210> 49
<211> 425
<212> PRT
<213> Chimpanzee Adenovirus- ChAd 4 Fiber

<400> 49

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Met Ser Lys Lys Arg Val Arg Val Asp Asp Asp Phe Asp Pro Val Tyr
 1               5                  10                  15
Pro Tyr Asp Ala Asp Asn Ala Pro Thr Val Pro Phe Ile Asn Pro Pro
            20                  25                  30
Phe Val Ser Ser Asp Gly Phe Gln Glu Lys Pro Leu Gly Val Leu Ser
        35                  40                  45
```

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Leu Arg Leu Ala Asp Pro Val Thr Thr Lys Asn Gly Glu Ile Thr Leu
    50                  55                  60
Lys Leu Gly Glu Gly Val Asp Leu Asp Ser Ser Gly Lys Leu Ile Ser
65                  70                  75                  80
Asn Thr Ala Thr Lys Ala Ala Ala Pro Leu Ser Phe Ser Asn Asn Thr
                85                  90                  95
Ile Ser Leu Asn Met Asp His Pro Phe Tyr Thr Lys Asp Gly Lys Leu
            100                 105                 110
Ser Leu Gln Val Ser Pro Pro Leu Asn Ile Leu Arg Thr Ser Ile Leu
        115                 120                 125
Asn Thr Leu Ala Leu Gly Phe Gly Ser Gly Leu Gly Leu Arg Gly Ser
    130                 135                 140
Ala Leu Ala Val Gln Leu Val Ser Pro Leu Thr Phe Asp Thr Asp Gly
145                 150                 155                 160
Asn Ile Lys Leu Thr Leu Asp Arg Gly Leu His Val Thr Thr Gly Asp
                165                 170                 175
Ala Ile Glu Ser Asn Ile Ser Trp Ala Lys Gly Leu Lys Phe Glu Asp
            180                 185                 190
Gly Ala Ile Ala Thr Asn Ile Gly Asn Gly Leu Glu Phe Gly Ser Ser
        195                 200                 205
Ser Thr Glu Thr Gly Val Asp Asp Ala Tyr Pro Ile Gln Val Lys Leu
    210                 215                 220
Gly Ser Gly Leu Ser Phe Asp Ser Thr Gly Ala Ile Met Ala Gly Asn
225                 230                 235                 240
Lys Glu Asp Asp Lys Leu Thr Leu Trp Thr Thr Pro Asp Pro Ser Pro
                245                 250                 255
Asn Cys Gln Ile Leu Ala Glu Asn Asp Ala Lys Leu Thr Leu Cys Leu
            260                 265                 270
Thr Lys Cys Gly Ser Gln Ile Leu Ala Thr Val Ser Val Leu Val Val
        275                 280                 285
Gly Ser Gly Asn Leu Asn Pro Ile Thr Gly Thr Val Ser Ser Ala Gln
    290                 295                 300
Val Phe Leu Arg Phe Asp Ala Asn Gly Val Leu Leu Thr Glu His Ser
305                 310                 315                 320
Thr Leu Lys Lys Tyr Trp Gly Tyr Arg Gln Gly Asp Ser Ile Asp Gly
                325                 330                 335
Thr Pro Tyr Thr Asn Ala Val Gly Phe Met Pro Asn Leu Lys Ala Tyr
            340                 345                 350
Pro Lys Ser Gln Ser Ser Thr Thr Lys Asn Asn Ile Val Gly Gln Val
        355                 360                 365
Tyr Met Asn Gly Asp Val Ser Lys Pro Met Leu Leu Thr Ile Thr Leu
    370                 375                 380
Asn Gly Thr Asp Asp Ser Asn Ser Thr Tyr Ser Met Ser Phe Ser Tyr
385                 390                 395                 400
Thr Trp Thr Asn Gly Ser Tyr Val Gly Ala Thr Phe Gly Ala Asn Ser
                405                 410                 415
Tyr Thr Phe Ser Tyr Ile Ala Gln Glu
            420                 425
```

<210> 50
<211> 444
<212> PRT
<213> Chimpanzee Adenovirus- ChAd 5 Fiber

<400> 50
Met Ser Lys Lys Arg Val Arg Val Asp Asp Asp Phe Asp Pro Val Tyr
1 5 10 15
Pro Tyr Asp Ala Asp Asn Ala Pro Thr Val Pro Phe Ile Asn Pro Pro
20 25 30
Phe Val Ser Ser Asp Gly Phe Gln Glu Lys Pro Leu Gly Val Leu Ser
35 40 45
Leu Arg Leu Ala Asp Pro Val Thr Thr Lys Asn Gly Glu Ile Thr Leu
50 55 60
Lys Leu Gly Asp Gly Val Asp Leu Asp Asp Ser Gly Lys Leu Ile Ser
65 70 75 80
Asn Thr Ala Thr Lys Ala Ala Ala Pro Leu Ser Phe Ser Asn Asn Thr
85 90 95
Ile Ser Leu Asn Met Asp Thr Pro Leu Tyr Asn Asn Asn Gly Lys Leu
100 105 110
Gly Met Lys Val Thr Ala Pro Leu Lys Ile Leu Asp Thr Asp Leu Leu
115 120 125
Lys Thr Leu Val Val Ala Tyr Gly Gln Gly Leu Gly Thr Asn Thr Asn
130 135 140
Gly Ala Leu Val Ala Gln Leu Ala Tyr Pro Leu Val Phe Asn Thr Ala
145 150 155 160
Ser Lys Ile Ala Leu Asn Leu Gly Asn Gly Pro Leu Lys Val Asp Ala
165 170 175
Asn Arg Leu Asn Ile Asn Cys Lys Arg Gly Ile Tyr Val Thr Thr Thr
180 185 190
Lys Asp Ala Leu Glu Ile Asn Ile Ser Trp Ala Asn Ala Met Thr Phe
195 200 205
Ile Gly Asn Ala Ile Gly Val Asn Ile Asp Thr Lys Lys Gly Leu Gln
210 215 220
Phe Gly Thr Ser Ser Thr Glu Thr Asp Val Lys Asn Ala Phe Ser Leu
225 230 235 240
Gln Val Lys Leu Gly Ala Gly Leu Thr Phe Asp Ser Thr Gly Ala Ile
245 250 255
Val Ala Trp Asn Lys Glu Asp Asp Lys Leu Thr Leu Trp Thr Thr Ala
260 265 270
Asp Pro Ser Pro Asn Cys His Ile Tyr Ser Ala Lys Asp Ala Lys Leu
275 280 285
Thr Leu Cys Leu Thr Lys Cys Gly Ser Gln Ile Leu Gly Thr Val Ser
290 295 300
Leu Leu Ala Val Ser Gly Ser Leu Ala Pro Ile Thr Gly Ala Val Arg
305 310 315 320
Thr Ala Leu Val Ser Leu Lys Phe Asn Ala Asn Gly Ala Leu Leu Asp
325 330 335
Lys Ser Thr Leu Asn Lys Glu Tyr Trp Asn Tyr Arg Gln Gly Asp Leu
340 345 350
Ile Pro Gly Thr Pro Tyr Thr His Ala Val Gly Phe Met Pro Asn Lys
355 360 365
Lys Ala Tyr Pro Lys Asn Thr Thr Ala Ala Ser Lys Ser His Ile Val
370 375 380
Gly Asp Val Tyr Leu Asp Gly Asp Ala Asp Lys Pro Leu Ser Leu Ile
385 390 395 400
Ile Thr Phe Asn Glu Thr Asp Asp Glu Thr Cys Asp Tyr Cys Ile Asn
405 410 415
Phe Gln Trp Lys Trp Gly Ala Asp Gln Tyr Lys Asp Lys Thr Leu Ala
420 425 430

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Thr Ser Ser Phe Thr Phe Ser Tyr Ile Ala Gln Glu
        435                 440


<210> 51
<211> 445
<212> PRT
<213> Chimpanzee Adenovirus- ChAd 7 Fiber

<400> 51
Met Ser Lys Lys Arg Val Arg Val Asp Asp Asp Phe Asp Pro Val Tyr
 1               5                  10                  15
Pro Tyr Asp Ala Asp Asn Ala Pro Thr Val Pro Phe Ile Asn Pro Pro
            20                  25                  30
Phe Val Ser Ser Asp Gly Phe Gln Glu Lys Pro Leu Gly Val Leu Ser
        35                  40                  45
Leu Arg Leu Ala Asp Pro Val Thr Thr Lys Asn Gly Glu Ile Thr Leu
    50                  55                  60
Lys Leu Gly Glu Gly Val Asp Leu Asp Ser Ser Gly Lys Leu Ile Ser
65                  70                  75                  80
Asn Thr Ala Thr Lys Ala Ala Ala Pro Leu Ser Phe Ser Asn Asn Thr
                85                  90                  95
Ile Ser Leu Asn Met Asp Thr Pro Phe Tyr Asn Asn Asn Gly Lys Leu
            100                 105                 110
Gly Met Lys Val Thr Ala Pro Leu Lys Ile Leu Asp Thr Asp Leu Leu
        115                 120                 125
Lys Thr Leu Val Val Ala Tyr Gly Gln Gly Leu Gly Thr Asn Thr Thr
    130                 135                 140
Gly Ala Leu Val Ala Gln Leu Ala Ala Pro Leu Ala Phe Asp Ser Asn
145                 150                 155                 160
Ser Lys Ile Ala Leu Asn Leu Gly Asn Gly Pro Leu Lys Val Asp Ala
                165                 170                 175
Asn Arg Leu Asn Ile Asn Cys Asn Arg Gly Leu Tyr Val Thr Thr Thr
            180                 185                 190
Lys Asp Ala Leu Glu Thr Asn Ile Ser Trp Ala Asn Ala Met Thr Phe
        195                 200                 205
Ile Gly Asn Ala Met Gly Val Asn Ile Asp Thr Gln Lys Gly Leu Gln
    210                 215                 220
Phe Gly Thr Thr Ser Thr Val Ala Asp Val Lys Asn Ala Tyr Pro Ile
225                 230                 235                 240
Gln Val Lys Leu Gly Ala Gly Leu Thr Phe Asp Ser Thr Gly Ala Ile
                245                 250                 255
Val Ala Trp Asn Lys Glu Asp Asp Lys Leu Thr Leu Trp Thr Thr Ala
            260                 265                 270
Asp Pro Ser Pro Asn Cys His Ile Tyr Ser Asp Lys Asp Ala Lys Leu
        275                 280                 285
Thr Leu Cys Leu Thr Lys Cys Gly Ser Gln Ile Leu Gly Thr Val Ser
    290                 295                 300
Leu Ile Ala Val Asp Thr Gly Ser Leu Asn Pro Ile Thr Gly Gln Val
305                 310                 315                 320
Thr Thr Ala Leu Val Ser Leu Lys Phe Asp Ala Asn Gly Val Leu Gln
                325                 330                 335
Thr Ser Ser Thr Leu Asp Lys Glu Tyr Trp Asn Phe Arg Lys Gly Asp
            340                 345                 350
Val Thr Pro Ala Glu Pro Tyr Thr Asn Ala Ile Gly Phe Met Pro Asn
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        355                 360                 365
Leu Lys Ala Tyr Pro Lys Asn Thr Ser Gly Ala Ala Lys Ser His Ile
    370                 375                 380
Val Gly Lys Val Tyr Leu His Gly Asp Thr Asp Lys Pro Leu Asp Leu
385                 390                 395                 400
Ile Ile Thr Phe Asn Glu Thr Ser Asp Glu Ser Cys Thr Tyr Cys Ile
                405                 410                 415
Asn Phe Gln Trp Lys Trp Asp Ser Thr Lys Tyr Thr Gly Glu Thr Leu
            420                 425                 430
Ala Thr Ser Ser Phe Thr Phe Ser Tyr Ile Ala Gln Glu
        435                 440                 445
```

<210> 52
<211> 425
<212> PRT
<213> Chimpanzee Adenovirus- ChAd 9 Fiber

<400> 52

```
Met Ser Lys Lys Arg Val Arg Val Asp Asp Asp Phe Asp Pro Val Tyr
 1               5                  10                  15
Pro Tyr Asp Ala Asp Asn Ala Pro Thr Val Pro Phe Ile Asn Pro Pro
            20                  25                  30
Phe Val Ser Ser Asp Gly Phe Gln Glu Lys Pro Leu Gly Val Leu Ser
        35                  40                  45
Leu Arg Leu Ala Asp Pro Val Thr Thr Lys Asn Gly Glu Ile Thr Leu
    50                  55                  60
Lys Leu Gly Glu Gly Val Asp Leu Asp Ser Ser Gly Lys Leu Ile Ser
65                  70                  75                  80
Asn Thr Ala Thr Lys Ala Ala Ala Pro Leu Ser Phe Ser Asn Asn Thr
                85                  90                  95
Ile Ser Leu Asn Met Asp His Pro Phe Tyr Thr Lys Asp Gly Lys Leu
            100                 105                 110
Ala Leu Gln Val Ser Pro Pro Leu Asn Ile Leu Arg Thr Ser Ile Leu
        115                 120                 125
Asn Thr Leu Ala Leu Gly Phe Gly Ser Gly Leu Gly Leu Arg Gly Ser
    130                 135                 140
Ala Leu Ala Val Gln Leu Val Ser Pro Leu Thr Phe Asp Thr Asp Gly
145                 150                 155                 160
Asn Ile Lys Leu Thr Leu Asp Arg Gly Leu His Val Thr Thr Gly Asp
                165                 170                 175
Ala Ile Glu Ser Asn Ile Ser Trp Ala Lys Gly Leu Lys Phe Glu Asp
            180                 185                 190
Gly Ala Ile Ala Thr Asn Ile Gly Asn Gly Leu Glu Phe Gly Ser Ser
        195                 200                 205
Ser Thr Glu Thr Gly Val Asp Asp Ala Tyr Pro Ile Gln Val Lys Leu
    210                 215                 220
Gly Ser Gly Leu Ser Phe Asp Ser Thr Gly Ala Ile Met Ala Gly Asn
225                 230                 235                 240
Lys Glu Asp Asp Lys Leu Thr Leu Trp Thr Thr Pro Asp Pro Ser Pro
                245                 250                 255
Asn Cys Gln Ile Leu Ala Glu Asn Asp Ala Lys Leu Thr Leu Cys Leu
            260                 265                 270
Thr Lys Cys Gly Ser Gln Ile Leu Ala Thr Val Ser Val Leu Val Val
        275                 280                 285
```

```
Gly Ser Gly Asp Leu Asn Pro Ile Thr Gly Thr Val Ser Ser Ala Gln
    290                 295                 300
Val Phe Leu Arg Phe Asp Ala Asn Gly Val Leu Leu Thr Glu His Ser
305                 310                 315                 320
Thr Leu Lys Lys Tyr Trp Gly Tyr Arg Gln Gly Asp Ser Ile Asp Gly
                325                 330                 335
Thr Pro Tyr Ala Asn Ala Val Gly Phe Met Pro Asn Leu Lys Ala Tyr
            340                 345                 350
Pro Lys Ser Gln Ser Ser Thr Thr Lys Asn Asn Ile Val Gly Gln Val
        355                 360                 365
Tyr Met Asn Gly Asp Val Ser Lys Pro Met Leu Leu Thr Ile Thr Leu
    370                 375                 380
Asn Gly Thr Asp Asp Ser Asn Ser Thr Tyr Ser Met Ser Phe Ser Tyr
385                 390                 395                 400
Thr Trp Thr Asn Gly Ser Tyr Val Gly Ala Thr Phe Gly Ala Asn Ser
                405                 410                 415
Tyr Thr Phe Ser Tyr Ile Ala Gln Glu
            420                 425
```

<210> 53
<211> 425
<212> PRT
<213> Chimpanzee Adenovirus- ChAd 10 Fiber

<400> 53

```
Met Ser Lys Lys Arg Val Arg Val Asp Asp Asp Phe Asp Pro Val Tyr
 1                5                  10                  15
Pro Tyr Asp Ala Asp Asn Ala Pro Thr Val Pro Phe Ile Asn Pro Pro
            20                  25                  30
Phe Val Ser Ser Asp Gly Phe Gln Glu Lys Pro Leu Gly Val Leu Ser
        35                  40                  45
Leu Arg Leu Ala Asp Pro Val Thr Thr Lys Asn Gly Glu Ile Thr Leu
    50                  55                  60
Lys Leu Gly Glu Gly Val Asp Leu Asp Ser Ser Gly Lys Leu Ile Ser
65                  70                  75                  80
Asn Thr Ala Thr Lys Ala Ala Ala Pro Leu Ser Phe Ser Asn Asn Thr
                85                  90                  95
Ile Ser Leu Asn Met Asp His Pro Phe Tyr Thr Lys Asp Gly Lys Leu
            100                 105                 110
Ser Leu Gln Val Ser Pro Pro Leu Asn Ile Leu Arg Thr Ser Ile Leu
        115                 120                 125
Asn Thr Leu Ala Leu Gly Phe Gly Ser Gly Leu Gly Leu Arg Gly Ser
    130                 135                 140
Ala Leu Ala Val Gln Leu Val Ser Pro Leu Thr Phe Asp Thr Asp Gly
145                 150                 155                 160
Asn Ile Lys Leu Thr Leu Asp Arg Gly Leu His Val Thr Thr Gly Asp
                165                 170                 175
Ala Ile Glu Ser Asn Ile Ser Trp Ala Lys Gly Leu Lys Phe Glu Asp
            180                 185                 190
Gly Ala Ile Ala Thr Asn Ile Gly Asn Gly Leu Glu Phe Gly Ser Ser
        195                 200                 205
Ser Thr Glu Thr Gly Val Asp Asp Ala Tyr Pro Ile Gln Val Lys Leu
    210                 215                 220
Gly Ser Gly Leu Ser Phe Asp Ser Thr Gly Ala Ile Met Ala Gly Asn
```

```
225                 230                 235                 240
Lys Glu Asp Asp Lys Leu Thr Leu Trp Thr Thr Pro Asp Pro Ser Pro
                245                 250                 255
Asn Cys Gln Ile Leu Ala Glu Asn Asp Ala Lys Leu Thr Leu Cys Leu
            260                 265                 270
Thr Lys Cys Gly Ser Gln Ile Leu Ala Thr Val Ser Val Leu Val Val
        275                 280                 285
Gly Ser Gly Asn Leu Asn Pro Ile Thr Gly Thr Val Ser Ser Ala Gln
    290                 295                 300
Val Phe Leu Arg Phe Asp Ala Asn Gly Val Leu Leu Thr Glu His Ser
305                 310                 315                 320
Thr Leu Lys Lys Tyr Trp Gly Tyr Arg Gln Gly Asp Ser Ile Asp Gly
                325                 330                 335
Thr Pro Tyr Thr Asn Ala Val Gly Phe Met Pro Asn Leu Lys Ala Tyr
            340                 345                 350
Pro Lys Ser Gln Ser Ser Thr Thr Lys Asn Asn Ile Val Gly Gln Val
        355                 360                 365
Tyr Met Asn Gly Asp Val Ser Lys Pro Met Leu Leu Thr Ile Thr Leu
    370                 375                 380
Asn Gly Thr Asp Asp Ser Asn Ser Thr Tyr Ser Met Ser Phe Ser Tyr
385                 390                 395                 400
Thr Trp Thr Asn Gly Ser Tyr Val Gly Ala Thr Phe Gly Ala Asn Ser
                405                 410                 415
Tyr Thr Phe Ser Tyr Ile Ala Gln Glu
            420                 425
```

<210> 54
<211> 578
<212> PRT
<213> Chimpanzee Adenovirus- ChAd 11 Fiber

<400> 54

```
Met Lys Arg Thr Lys Thr Ser Asp Glu Ser Phe Asn Pro Val Tyr Pro
 1               5                  10                  15
Tyr Asp Thr Glu Asn Gly Pro Pro Ser Val Pro Phe Leu Thr Pro Pro
            20                  25                  30
Phe Val Ser Pro Asp Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser
        35                  40                  45
Leu Asn Leu Ala Glu Pro Leu Val Thr Ser His Gly Met Leu Ala Leu
    50                  55                  60
Lys Met Gly Ser Gly Leu Ser Leu Asp Asp Ala Gly Asn Leu Thr Ser
65                  70                  75                  80
Gln Asp Val Thr Thr Thr Thr Pro Pro Leu Lys Lys Thr Lys Thr Asn
                85                  90                  95
Leu Ser Leu Glu Thr Ser Ala Pro Leu Thr Val Ser Thr Ser Gly Ala
            100                 105                 110
Leu Thr Leu Ala Ala Ala Val Pro Leu Ala Val Ala Gly Thr Ser Leu
        115                 120                 125
Thr Met Gln Ser Glu Ala Pro Leu Thr Val Gln Asp Ala Lys Leu Thr
    130                 135                 140
Leu Ala Thr Lys Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu
145                 150                 155                 160
Gln Thr Ser Ala Pro Leu Thr Ala Ala Asp Ser Ser Thr Leu Thr Ile
                165                 170                 175
```

```
Ser Ala Thr Pro Pro Leu Ser Thr Ser Asn Gly Ser Leu Gly Ile Asp
            180                 185                 190
Met Gln Ala Pro Ile Tyr Thr Thr Asn Gly Lys Leu Gly Leu Asn Phe
        195                 200                 205
Gly Ala Pro Leu His Val Val Asp Ser Leu Asn Ala Leu Thr Val Val
    210                 215                 220
Thr Gly Gln Gly Leu Thr Ile Asn Gly Thr Ala Leu Gln Thr Arg Val
225                 230                 235                 240
Ser Gly Ala Leu Asn Tyr Asp Ser Ser Gly Asn Leu Glu Leu Arg Ala
                245                 250                 255
Ala Gly Gly Met Arg Val Asp Ala Asn Gly Lys Leu Ile Leu Asp Val
            260                 265                 270
Ala Tyr Pro Phe Asp Ala Gln Asn Asn Leu Ser Leu Arg Leu Gly Gln
        275                 280                 285
Gly Pro Leu Phe Val Asn Ser Ala His Asn Leu Asp Val Asn Tyr Asn
    290                 295                 300
Arg Gly Leu Tyr Leu Phe Thr Ser Gly Asn Thr Lys Lys Leu Glu Val
305                 310                 315                 320
Asn Ile Lys Thr Ala Lys Gly Leu Ile Tyr Asp Asp Thr Ala Ile Ala
                325                 330                 335
Ile Asn Pro Gly Asp Gly Leu Glu Phe Gly Ser Gly Ser Asp Thr Asn
            340                 345                 350
Pro Leu Lys Thr Lys Leu Gly Leu Gly Leu Glu Tyr Asp Ser Ser Arg
        355                 360                 365
Ala Ile Ile Ala Lys Leu Gly Thr Gly Leu Ser Phe Asp Asn Thr Gly
    370                 375                 380
Ala Ile Thr Val Gly Asn Lys Asn Asp Asp Lys Leu Thr Leu Trp Thr
385                 390                 395                 400
Thr Pro Asp Pro Ser Pro Asn Cys Arg Ile Tyr Ser Glu Lys Asp Ala
                405                 410                 415
Lys Phe Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Val Leu Ala Ser
            420                 425                 430
Val Ser Val Leu Ser Val Lys Gly Ser Leu Ala Pro Ile Ser Gly Thr
        435                 440                 445
Val Thr Ser Ala Gln Ile Ile Leu Arg Phe Asp Glu Asn Gly Val Leu
    450                 455                 460
Leu Ser Asn Ser Ser Leu Asp Pro Gln Tyr Trp Asn Tyr Arg Lys Gly
465                 470                 475                 480
Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly Phe Met Pro
                485                 490                 495
Asn Leu Thr Ala Tyr Pro Lys Thr Gln Ser Gln Thr Ala Lys Ser Asn
            500                 505                 510
Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Ser Lys Pro Met Ile
        515                 520                 525
Leu Thr Ile Thr Leu Asn Gly Thr Asn Glu Thr Gly Asp Ala Thr Val
    530                 535                 540
Ser Thr Tyr Ser Met Ser Phe Ser Trp Asn Trp Asn Gly Ser Asn Tyr
545                 550                 555                 560
Ile Asn Glu Thr Phe Gln Thr Asn Ser Phe Thr Phe Ser Tyr Ile Ala
                565                 570                 575
Gln Glu
```

<210> 55

<211> 442
<212> PRT
<213> Chimpansee Adenovirus- ChAd 16 Fiber

<400> 55
Met Ser Lys Lys Arg Val Arg Val Asp Asp Asp Phe Asp Pro Val Tyr
 1   5   10   15
Pro Tyr Asp Ala Asp Asn Ala Pro Thr Val Pro Phe Ile Asn Pro Pro
            20   25   30
Phe Val Ser Ser Asp Gly Phe Gln Glu Lys Pro Leu Gly Val Leu Ser
        35   40   45
Leu Arg Leu Ala Asp Pro Val Thr Thr Lys Asn Gly Glu Ile Thr Leu
    50   55   60
Lys Leu Gly Glu Gly Val Asp Leu Asp Ser Ser Gly Lys Leu Ile Ser
65   70   75   80
Asn Thr Ala Thr Lys Ala Ala Ala Pro Leu Ser Phe Ser Asn Asn Thr
                85   90   95
Ile Ser Leu Asn Met Asp Thr Pro Phe Tyr Thr Lys Asp Gly Lys Leu
            100   105   110
Thr Met Gln Val Thr Ala Pro Leu Lys Leu Ala Asn Thr Ala Ile Leu
        115   120   125
Asn Thr Leu Ala Met Ala Tyr Gly Asn Gly Leu Gly Leu Ser Asn Asn
    130   135   140
Ala Leu Thr Val Gln Leu Gln Ser Pro Leu Thr Phe Asn Asn Ser Lys
145   150   155   160
Val Ala Ile Asn Leu Gly Asn Gly Pro Leu Asn Val Thr Ser Asn Arg
                165   170   175
Leu Ser Ile Asn Cys Lys Arg Gly Val Tyr Val Thr Thr Thr Gly Asp
            180   185   190
Ala Ile Glu Thr Asn Ile Ser Trp Ser Asn Ala Ile Lys Phe Ile Gly
        195   200   205
Asn Ala Met Gly Val Asn Ile Asp Thr Asn Lys Gly Leu Gln Phe Gly
    210   215   220
Thr Thr Ser Thr Val Thr Asp Val Thr Asn Ala Phe Pro Ile Gln Val
225   230   235   240
Lys Leu Gly Ala Gly Leu Ala Phe Asp Ser Thr Gly Ala Ile Val Ala
                245   250   255
Trp Asn Lys Glu Asp Asp Ser Leu Thr Leu Trp Thr Thr Pro Asp Pro
            260   265   270
Ser Pro Asn Cys Lys Ile Ala Ser Asp Lys Asp Ala Lys Leu Thr Leu
        275   280   285
Cys Leu Thr Lys Cys Gly Ser Gln Ile Leu Gly Thr Val Ser Leu Leu
    290   295   300
Ala Val Ser Gly Ser Leu Ala Pro Ile Thr Gly Ala Val Ser Thr Ala
305   310   315   320
Leu Val Ser Leu Lys Phe Asp Ala Asn Gly Ala Leu Leu Glu Lys Ser
                325   330   335
Thr Leu Asn Arg Glu Tyr Trp Asn Tyr Arg Gln Gly Asp Leu Ile Pro
            340   345   350
Gly Thr Pro Tyr Thr His Ala Val Gly Phe Met Pro Asn Lys Lys Ala
        355   360   365
Tyr Pro Lys Asn Thr Thr Ala Ala Ser Lys Ser His Ile Val Gly Glu
    370   375   380
Val Tyr Leu Asp Gly Asp Ala Asp Lys Pro Leu Ser Leu Ile Ile Thr
385   390   395   400

```
Phe Asn Glu Thr Asp Asp Glu Ser Cys Asp Tyr Cys Met Asn Phe Gln
                405                 410                 415
Trp Lys Trp Gly Ala Asp Gln Tyr Lys Asp Lys Thr Leu Ala Thr Ser
            420                 425                 430
Ser Phe Thr Phe Ser Tyr Ile Ala Gln Glu
        435                 440
```

<210> 56
<211> 543
<212> PRT
<213> Chimpanzee Adenovirus- ChAd 17 Fiber

<400> 56

```
Met Lys Arg Thr Lys Thr Ser Asp Glu Ser Phe Asn Pro Val Tyr Pro
 1               5                  10                  15
Tyr Asp Thr Glu Ser Gly Pro Pro Ser Val Pro Phe Leu Thr Pro Pro
            20                  25                  30
Phe Val Ser Pro Asp Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser
        35                  40                  45
Leu Asn Leu Ala Glu Pro Leu Val Thr Ser His Gly Met Leu Ala Leu
    50                  55                  60
Lys Met Gly Ser Gly Leu Ser Leu Asp Asp Ala Gly Asn Leu Thr Ser
65                  70                  75                  80
Gln Asp Ile Thr Ser Thr Thr Pro Pro Leu Lys Lys Thr Lys Thr Asn
                85                  90                  95
Leu Ser Leu Glu Thr Ser Ser Pro Leu Thr Val Ser Thr Ser Gly Ala
            100                 105                 110
Leu Thr Val Ala Ala Ala Ala Pro Leu Ala Val Ala Gly Thr Ser Leu
        115                 120                 125
Thr Met Gln Ser Glu Ala Pro Leu Ala Val Gln Asp Ala Lys Leu Thr
    130                 135                 140
Leu Ala Thr Lys Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu
145                 150                 155                 160
Gln Thr Ser Ala Pro Leu Thr Ala Ala Asp Ser Ser Thr Leu Thr Val
                165                 170                 175
Ser Ser Thr Pro Pro Ile Ser Val Ser Ser Gly Ser Leu Gly Leu Asp
            180                 185                 190
Met Glu Asp Pro Met Tyr Thr His Asp Gly Lys Leu Gly Ile Arg Ile
        195                 200                 205
Gly Gly Pro Leu Arg Val Val Asp Ser Leu His Thr Leu Thr Val Val
    210                 215                 220
Thr Gly Asn Gly Leu Thr Val Asp Asn Asn Ala Leu Gln Thr Arg Val
225                 230                 235                 240
Thr Gly Ala Leu Gly Tyr Asp Thr Ser Gly Asn Leu Gln Leu Arg Ala
                245                 250                 255
Ala Gly Gly Met Arg Ile Asp Ala Asn Gly Gln Leu Ile Leu Asp Val
            260                 265                 270
Ala Tyr Pro Phe Asp Ala Gln Asn Asn Leu Ser Leu Arg Leu Gly Gln
        275                 280                 285
Gly Pro Leu Tyr Val Asn Thr Asp His Asn Leu Asp Leu Asn Cys Asn
    290                 295                 300
Arg Gly Leu Thr Thr Thr Thr Thr Asn Asn Thr Lys Lys Leu Glu Thr
305                 310                 315                 320
Lys Ile Ser Ser Gly Leu Asp Tyr Asp Thr Asn Gly Ala Val Ile Ile
```

```
                325                 330                 335
Lys Leu Gly Thr Gly Leu Ser Phe Asp Asn Thr Gly Ala Leu Thr Val
            340                 345                 350
Gly Asn Thr Gly Asp Asp Lys Leu Thr Leu Trp Thr Thr Pro Asp Pro
        355                 360                 365
Ser Pro Asn Cys Arg Ile His Ser Asp Lys Asp Cys Lys Phe Thr Leu
    370                 375                 380
Val Leu Thr Lys Cys Gly Ser Gln Ile Leu Ala Ser Val Ala Ala Leu
385                 390                 395                 400
Ala Val Ser Gly Asn Leu Ala Ser Ile Thr Gly Thr Val Ala Ser Val
                405                 410                 415
Thr Ile Phe Leu Arg Phe Asp Gln Asn Gly Val Leu Met Glu Asn Ser
            420                 425                 430
Ser Leu Asp Lys Gln Tyr Trp Asn Phe Arg Asn Gly Asn Ser Thr Asn
        435                 440                 445
Ala Ala Pro Tyr Thr Asn Ala Val Gly Phe Met Pro Asn Leu Ala Ala
    450                 455                 460
Tyr Pro Lys Thr Gln Ser Gln Thr Ala Lys Asn Asn Ile Val Ser Gln
465                 470                 475                 480
Val Tyr Leu Asn Gly Asp Lys Ser Lys Pro Met Thr Leu Thr Ile Thr
                485                 490                 495
Leu Asn Gly Thr Asn Glu Ser Ser Glu Thr Ser Gln Val Ser His Tyr
            500                 505                 510
Ser Met Ser Phe Thr Trp Ala Trp Glu Ser Gly Gln Tyr Ala Thr Glu
        515                 520                 525
Thr Phe Ala Thr Asn Ser Phe Thr Phe Ser Tyr Ile Ala Glu Gln
    530                 535                 540
```

<210> 57
<211> 543
<212> PRT
<213> Chimpanzee Adenovirus- ChAd 19 Fiber

<400> 57

```
Met Lys Arg Thr Lys Thr Ser Asp Lys Ser Phe Asn Pro Val Tyr Pro
 1                5                  10                  15
Tyr Asp Thr Glu Asn Gly Pro Pro Ser Val Pro Phe Leu Thr Pro Pro
            20                  25                  30
Phe Val Ser Pro Asp Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser
        35                  40                  45
Leu Asn Leu Ala Glu Pro Leu Val Thr Ser His Gly Met Leu Ala Leu
    50                  55                  60
Lys Met Gly Ser Gly Leu Ser Leu Asp Asp Ala Gly Asn Leu Thr Ser
65                  70                  75                  80
Gln Asp Val Thr Thr Thr Thr Pro Pro Leu Lys Lys Thr Lys Thr Asn
                85                  90                  95
Leu Ser Leu Glu Thr Ser Ala Pro Leu Thr Val Ser Thr Ser Gly Ala
            100                 105                 110
Leu Thr Leu Ala Ala Ala Ala Pro Leu Ala Val Ala Gly Thr Ser Leu
        115                 120                 125
Thr Met Gln Ser Glu Ala Pro Leu Thr Val Gln Asp Ala Lys Leu Thr
    130                 135                 140
Leu Ala Thr Lys Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu
145                 150                 155                 160
```

```
Gln Thr Ser Ala Pro Leu Thr Ala Ala Asp Ser Ser Thr Leu Thr Val
                165                 170                 175
Ser Ala Thr Pro Pro Ile Ser Val Ser Ser Gly Ser Leu Gly Leu Asp
            180                 185                 190
Met Glu Asp Pro Met Tyr Thr His Asp Gly Lys Leu Gly Ile Arg Ile
        195                 200                 205
Gly Gly Pro Leu Arg Val Val Asp Ser Leu His Thr Leu Thr Val Val
    210                 215                 220
Thr Gly Asn Gly Ile Ala Val Asp Asn Asn Ala Leu Gln Thr Arg Val
225                 230                 235                 240
Thr Gly Ala Leu Gly Tyr Asp Thr Ser Gly Asn Leu Gln Leu Arg Ala
                245                 250                 255
Ala Gly Gly Met Arg Ile Asp Ala Asn Gly Gln Leu Ile Leu Asp Val
            260                 265                 270
Ala Tyr Pro Phe Asp Ala Gln Asn Asn Leu Ser Leu Arg Leu Gly Gln
        275                 280                 285
Gly Pro Leu Tyr Val Asn Thr Asp His Asn Leu Asp Leu Asn Cys Asn
    290                 295                 300
Arg Gly Leu Thr Thr Thr Thr Thr Asn Asn Thr Lys Lys Leu Glu Thr
305                 310                 315                 320
Lys Ile Gly Ser Gly Leu Asp Tyr Asp Thr Asn Gly Ala Val Ile Ile
                325                 330                 335
Lys Leu Gly Thr Gly Val Ser Phe Asp Ser Thr Gly Ala Leu Ser Val
            340                 345                 350
Gly Asn Thr Gly Asp Asp Lys Leu Thr Leu Trp Thr Thr Pro Asp Pro
        355                 360                 365
Ser Pro Asn Cys Arg Ile His Ser Asp Lys Asp Cys Lys Phe Thr Leu
    370                 375                 380
Val Leu Thr Lys Cys Gly Ser Gln Ile Leu Ala Ser Val Ala Ala Leu
385                 390                 395                 400
Ala Val Ser Gly Asn Leu Ala Ser Ile Thr Gly Thr Val Ser Ser Val
                405                 410                 415
Thr Ile Phe Leu Arg Phe Asp Gln Asn Gly Val Leu Met Glu Asn Ser
            420                 425                 430
Ser Leu Asp Lys Gln Tyr Trp Asn Phe Arg Asn Gly Asn Ser Thr Asn
        435                 440                 445
Ala Thr Pro Tyr Thr Asn Ala Val Gly Phe Met Pro Asn Leu Ala Ala
    450                 455                 460
Tyr Pro Lys Thr Gln Ser Gln Thr Ala Lys Asn Asn Ile Val Ser Gln
465                 470                 475                 480
Val Tyr Leu Asn Gly Asp Lys Ser Lys Pro Met Thr Leu Thr Ile Thr
                485                 490                 495
Leu Asn Gly Thr Asn Glu Ser Ser Glu Thr Ser Gln Val Ser His Tyr
            500                 505                 510
Ser Met Ser Phe Thr Trp Ala Trp Glu Ser Gly Gln Tyr Ala Thr Glu
        515                 520                 525
Thr Phe Ala Thr Asn Ser Phe Thr Phe Ser Tyr Ile Ala Glu Gln
    530                 535                 540
```

<210> 58
<211> 963
<212> DNA
<213> Chimapnzee Adenovirus- ChAd 8 Fiber

<400> 58
atgaccaaac gagttcgact aagcagctcc ttcaatccgg tctaccccta tgaagatgaa 60
agcagctccc aacacccctt tataaaccct ggtttcattt cctcaaatgg atttacacaa 120
agcccagatg gggttcttac acttaaatgc ttatcgccgc tcaccaccac aggcggctcc 180
cttcaactta aagttggagg aggattatca gtggatgaca ctgacggttc attagaagaa 240
aacataagca ttacagcacc acttaataaa acaagtcact caataggttt atccatagga 300
gatgggttgg aaacaaaaaa caaccaacta tgtgctaagc tgggagacgg tcttacattt 360
aatacaggca gcatatgcat agatactgac attaatacat tatggacagg agcaacacca 420
gacgctaatt gcttagtcct tggaactgaa tctaatgatt gtaaacttac actggcactt 480
gtaaagtcag gagccttagt aaatgcttac gtagcacttg ttggagcctc agacgccgtt 540
aatgatttaa ccacagaaac aagtgctcaa ataattgcag acatatattt tgatgcgcaa 600
ggaaaacttc ttcctgattt atcagcactc aaaacagagc taaaacacaa atctggacaa 660
ggcacttcga cagcagatcc caataactgt aaaagcttta tgccaagtct aaatgcatat 720
ccactgcgcc ccaatggagg caacggaaac tatatttatg gaaccaccta ctacagggcc 780
agagatgaaa ccctttatga acttaaaacc tctgtaatgc ttaactacaa aattaccagt 840
ggactatgtg catatgccat gcattttcag tggtcttgga atagtgggac taaaccagaa 900
gacactcccg ccactttcat tgcctccccc tttgtctttt cctacattag agaagatgac 960
tga 963

<210> 59
<211> 320
<212> PRT
<213> Chimpanzee Adenovirus- ChAd 8 Fiber

<400> 59
Met Thr Lys Arg Val Arg Leu Ser Ser Ser Phe Asn Pro Val Tyr Pro
 1   5   10   15
Tyr Glu Asp Glu Ser Ser Ser Gln His Pro Phe Ile Asn Pro Gly Phe
            20   25   30
Ile Ser Ser Asn Gly Phe Thr Gln Ser Pro Asp Gly Val Leu Thr Leu
        35   40   45
Lys Cys Leu Ser Pro Leu Thr Thr Thr Gly Gly Ser Leu Gln Leu Lys
    50   55   60
Val Gly Gly Gly Leu Ser Val Asp Asp Thr Asp Gly Ser Leu Glu Glu
65   70   75   80
Asn Ile Ser Ile Thr Ala Pro Leu Asn Lys Thr Ser His Ser Ile Gly
                85   90   95
Leu Ser Ile Gly Asp Gly Leu Glu Thr Lys Asn Asn Gln Leu Cys Ala
            100   105   110
Lys Leu Gly Asp Gly Leu Thr Phe Asn Thr Gly Ser Ile Cys Ile Asp
        115   120   125
Thr Asp Ile Asn Thr Leu Trp Thr Gly Ala Thr Pro Asp Ala Asn Cys
    130   135   140
Leu Val Leu Gly Thr Glu Ser Asn Asp Cys Lys Leu Thr Leu Ala Leu
145   150   155   160
Val Lys Ser Gly Ala Leu Val Asn Ala Tyr Val Ala Leu Val Gly Ala
                165   170   175
Ser Asp Ala Val Asn Asp Leu Thr Thr Glu Thr Ser Ala Gln Ile Ile
            180   185   190
Ala Asp Ile Tyr Phe Asp Ala Gln Gly Lys Leu Leu Pro Asp Leu Ser
        195   200   205
Ala Leu Lys Thr Glu Leu Lys His Lys Ser Gly Gln Gly Thr Ser Thr
    210   215   220
Ala Asp Pro Asn Asn Cys Lys Ser Phe Met Pro Ser Leu Asn Ala Tyr
225   230   235   240

```
Pro Leu Arg Pro Asn Gly Gly Asn Gly Asn Tyr Ile Tyr Gly Thr Thr
                245                 250                 255
Tyr Tyr Arg Ala Arg Asp Glu Thr Leu Tyr Glu Leu Lys Thr Ser Val
            260                 265                 270
Met Leu Asn Tyr Lys Ile Thr Ser Gly Leu Cys Ala Tyr Ala Met His
        275                 280                 285
Phe Gln Trp Ser Trp Asn Ser Gly Thr Lys Pro Glu Asp Thr Pro Ala
    290                 295                 300
Thr Phe Ile Ala Ser Pro Phe Val Phe Ser Tyr Ile Arg Glu Asp Asp
305                 310                 315                 320
```

<210> 60
<211> 1062
<212> DNA
<213> Chimpanzee Adenovirus- ChAd 22 Fiber

<400> 60

```
atggccaaac gagctcggct aagcagctcc ttcaatccgg tctaccccta tgaagatgaa 60
agcagctcac aacacccctt tataaaccct ggtttcattt cctcaaatgg ttttgcacaa 120
agcccagatg gagttctaac tcttaaatgt gttaatccgc tcactaccgc cagcggaccc 180
ctccaactta aagttggaag cagtcttaca gtagataata tcgatgggtc tttggaggaa 240
aatataactg ccgcagcgcc actcactaaa actaaccact ccataggttt atcaatagga 300
tctggcttgc aaacaaagga tgataaactt tgtttatcgc tgggagatgg gttggtaaca 360
aaggatgata aactatgttt atcgctggga gatgggttaa taacaaaaga tgatacacta 420
tgtgccaaac taggacatgg ccttgtgttt gactcttcca atgctatcac catagaaaac 480
aacaccttgt ggacaggtgc aaaaccaagc gccaactgtg taattaaaga gggagaagat 540
tccccagact gtaagctcac tttagttcta gtgaagaatg gaggactgat aaatggatac 600
ataacattaa tgggagcctc agaatatact aacaccttgt ttaaaaacaa acaagttaca 660
atcgatgtaa acctcgcatt tgataatact ggccaaatta tcacttacct atcatccctt 720
aaaagtaacc tgaactttaa agacaaccaa aacatggcta ctggaaccat aaccagtgcc 780
aaaggcttca tgcccagcac caccgcctat ccatttataa catacgccac tcagtcccta 840
aatgaagatt acatttatgg agagtgttac tacaaatcta ccaatggaac tctctttcca 900
ctaaaagtta ctgtcacact aaacagacgt atgtcagctt ctggaatggc ctatgctatg 960
aatttttcat ggtctctaaa tgcagaggaa gccccggaaa ctaccgaagt cactctcatt 1020
acctcccccc tctttttttc ttatatcaga gaagatgact ga                    1062
```

<210> 61
<211> 353
<212> PRT
<213> Chimpanzee Adenovirus- ChAd 22 Fiber

<400> 61

```
Met Ala Lys Arg Ala Arg Leu Ser Ser Ser Phe Asn Pro Val Tyr Pro
 1               5                  10                  15
Tyr Glu Asp Glu Ser Ser Ser Gln His Pro Phe Ile Asn Pro Gly Phe
            20                  25                  30
Ile Ser Ser Asn Gly Phe Ala Gln Ser Pro Asp Gly Val Leu Thr Leu
        35                  40                  45
Lys Cys Val Asn Pro Leu Thr Thr Ala Ser Gly Pro Leu Gln Leu Lys
    50                  55                  60
Val Gly Ser Ser Leu Thr Val Asp Asn Ile Asp Gly Ser Leu Glu Glu
65                  70                  75                  80
Asn Ile Thr Ala Ala Ala Pro Leu Thr Lys Thr Asn His Ser Ile Gly
                85                  90                  95
```

```
Leu Ser Ile Gly Ser Gly Leu Gln Thr Lys Asp Asp Lys Leu Cys Leu
            100                 105                 110
Ser Leu Gly Asp Gly Leu Val Thr Lys Asp Asp Lys Leu Cys Leu Ser
        115                 120                 125
Leu Gly Asp Gly Leu Ile Thr Lys Asp Asp Thr Leu Cys Ala Lys Leu
    130                 135                 140
Gly His Gly Leu Val Phe Asp Ser Ser Asn Ala Ile Thr Ile Glu Asn
145                 150                 155                 160
Asn Thr Leu Trp Thr Gly Ala Lys Pro Ser Ala Asn Cys Val Ile Lys
                165                 170                 175
Glu Gly Glu Asp Ser Pro Asp Cys Lys Leu Thr Leu Val Leu Val Lys
            180                 185                 190
Asn Gly Gly Leu Ile Asn Gly Tyr Ile Thr Leu Met Gly Ala Ser Glu
        195                 200                 205
Tyr Thr Asn Thr Leu Phe Lys Asn Lys Gln Val Thr Ile Asp Val Asn
    210                 215                 220
Leu Ala Phe Asp Asn Thr Gly Gln Ile Ile Thr Tyr Leu Ser Ser Leu
225                 230                 235                 240
Lys Ser Asn Leu Asn Phe Lys Asp Asn Gln Asn Met Ala Thr Gly Thr
                245                 250                 255
Ile Thr Ser Ala Lys Gly Phe Met Pro Ser Thr Thr Ala Tyr Pro Phe
            260                 265                 270
Ile Thr Tyr Ala Thr Gln Ser Leu Asn Glu Asp Tyr Ile Tyr Gly Glu
        275                 280                 285
Cys Tyr Tyr Lys Ser Thr Asn Gly Thr Leu Phe Pro Leu Lys Val Thr
    290                 295                 300
Val Thr Leu Asn Arg Arg Met Ser Ala Ser Gly Met Ala Tyr Ala Met
305                 310                 315                 320
Asn Phe Ser Trp Ser Leu Asn Ala Glu Glu Ala Pro Glu Thr Thr Glu
                325                 330                 335
Val Thr Leu Ile Thr Ser Pro Phe Phe Phe Ser Tyr Ile Arg Glu Asp
            340                 345                 350
Asp
```

<210> 62
<211> 1686
<212> DNA
<213> Chimpanzee Adenovirus- ChAd 24 Fiber

<400> 62
atgtcagatt cttgctcctg tccttccgca cccactatct tcatgttgtt gcagatgaag 60
cgcaccaaaa cgtctgacga gagcttcaac cccgtgtacc cctatgacac ggaaaacggt 120
cctccctccg tccctttcct caccctccc ttcgtgtctc ccgatggatt ccaagagagc 180
ccccccgggg tcctgtctct gaacctggcc gagcccctgg tcacttccca cggcatgctc 240
gccctgaaaa tgggaagtgg cctctccctg gacgacgccg gcaacctcac ctctcaagat 300
gtcaccacca ctacccctcc cctgaaaaaa accaagacca acctcagcct agaaacctca 360
gccccccctga ctgtgagcac ctcaggcgcc ctcaccctag cggccgccgc tcccctggcg 420
gtggccggca cctccctcac catgcaatca gaggcccccc tgacagtaca ggatgcaaaa 480
ctcaccctgg ccaccaaggg ccccctgacc gtgtctgaag gcaaactggc cttgcagacc 540
tcggccccac tgacggccgc tgacagcagc accctcaccg ttagcgccac accacccatc 600
aatgtaagca gtggaagttt gggcttagac atggaaaatc ccatgtatac tcatgacgga 660
aaactgggaa taagaattgg gggcccactg agagtagtag acagcctgca cacactgact 720
gtagttaccg gaaatggaat agctgtagat aacaatgccc tccaaactag agttacgggc 780

```
gccctgggtt atgacacatc aggaaaccta caactgagag ccgcgggggg tatgcgaatt 840
gatgcaaatg gccaacttat ccttgatgtg gcatacccat ttgatgctca aaacaatctc 900
agccttagac ttggtcaggg acccctgtat gtaaacacag accacaacct agatttgaat 960
tgcaacagag gtctgaccac aactaccacc aacaacacaa aaaaacttga aactaaaatt 1020
ggctcaggct tagactatga taccaatggt gctgtcatta ttaaacttgg cactggtgtc 1080
agctttgaca gcacaggcgc cctaagtgtg ggaaacactg gcgatgataa actgactctg 1140
tggacaaccc cagacccatc tccaaattgc agaattcact cagacaaaga ctgcaagttt 1200
actctagtcc taactaagtg tggaagtcaa atcctggctt ctgtcgccgc cctagcggtg 1260
tcaggaaatc tggcttcaat aacaggcacc gtttccagcg ttaccatctt tctcagattt 1320
gatcagaatg gagtgcttat ggaaaactcc tcgctagaca agcagtactg gaactttaga 1380
aatggtaatt caaccaatgc cacccctac accaatgcag ttggtttcat gccaaacctc 1440
gcagcatacc ccaagacaca gagtcagact gctaaaaaca acattgtaag tcaggtttac 1500
ttgaatgggg acaaatccaa acccatgatc cttaccatta ccctcaatgg aactaatgaa 1560
tccagtgaaa ctagccaggt gagtcactac tccatgtcat ttacgtgggc ttgggagagt 1620
gggcaatatg ccaccgaaac ctttgccacc aattccttta ccttctctta cattgctgaa 1680
caataa                                                           1686
```

<210> 63
<211> 543
<212> PRT
<213> Chimpanzee Adenovirus- ChAd 24 Fiber

<400> 63

```
Met Lys Arg Thr Lys Thr Ser Asp Glu Ser Phe Asn Pro Val Tyr Pro
 1               5                  10                  15
Tyr Asp Thr Glu Asn Gly Pro Pro Ser Val Pro Phe Leu Thr Pro Pro
            20                  25                  30
Phe Val Ser Pro Asp Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser
        35                  40                  45
Leu Asn Leu Ala Glu Pro Leu Val Thr Ser His Gly Met Leu Ala Leu
    50                  55                  60
Lys Met Gly Ser Gly Leu Ser Leu Asp Asp Ala Gly Asn Leu Thr Ser
65                  70                  75                  80
Gln Asp Val Thr Thr Thr Thr Pro Pro Leu Lys Lys Thr Lys Thr Asn
                85                  90                  95
Leu Ser Leu Glu Thr Ser Ala Pro Leu Thr Val Ser Thr Ser Gly Ala
            100                 105                 110
Leu Thr Leu Ala Ala Ala Ala Pro Leu Ala Val Ala Gly Thr Ser Leu
        115                 120                 125
Thr Met Gln Ser Glu Ala Pro Leu Thr Val Gln Asp Ala Lys Leu Thr
    130                 135                 140
Leu Ala Thr Lys Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu
145                 150                 155                 160
Gln Thr Ser Ala Pro Leu Thr Ala Ala Asp Ser Ser Thr Leu Thr Val
                165                 170                 175
Ser Ala Thr Pro Pro Ile Asn Val Ser Ser Gly Ser Leu Gly Leu Asp
            180                 185                 190
Met Glu Asn Pro Met Tyr Thr His Asp Gly Lys Leu Gly Ile Arg Ile
        195                 200                 205
Gly Gly Pro Leu Arg Val Val Asp Ser Leu His Thr Leu Thr Val Val
    210                 215                 220
Thr Gly Asn Gly Ile Ala Val Asp Asn Asn Ala Leu Gln Thr Arg Val
225                 230                 235                 240
Thr Gly Ala Leu Gly Tyr Asp Thr Ser Gly Asn Leu Gln Leu Arg Ala
                245                 250                 255
```

```
Ala Gly Gly Met Arg Ile Asp Ala Asn Gly Gln Leu Ile Leu Asp Val
            260                 265                 270
Ala Tyr Pro Phe Asp Ala Gln Asn Asn Leu Ser Leu Arg Leu Gly Gln
        275                 280                 285
Gly Pro Leu Tyr Val Asn Thr Asp His Asn Leu Asp Leu Asn Cys Asn
    290                 295                 300
Arg Gly Leu Thr Thr Thr Thr Thr Asn Asn Thr Lys Lys Leu Glu Thr
305                 310                 315                 320
Lys Ile Gly Ser Gly Leu Asp Tyr Asp Thr Asn Gly Ala Val Ile Ile
                325                 330                 335
Lys Leu Gly Thr Gly Val Ser Phe Asp Ser Thr Gly Ala Leu Ser Val
            340                 345                 350
Gly Asn Thr Gly Asp Asp Lys Leu Thr Leu Trp Thr Thr Pro Asp Pro
        355                 360                 365
Ser Pro Asn Cys Arg Ile His Ser Asp Lys Asp Cys Lys Phe Thr Leu
    370                 375                 380
Val Leu Thr Lys Cys Gly Ser Gln Ile Leu Ala Ser Val Ala Ala Leu
385                 390                 395                 400
Ala Val Ser Gly Asn Leu Ala Ser Ile Thr Gly Thr Val Ser Ser Val
                405                 410                 415
Thr Ile Phe Leu Arg Phe Asp Gln Asn Gly Val Leu Met Glu Asn Ser
            420                 425                 430
Ser Leu Asp Lys Gln Tyr Trp Asn Phe Arg Asn Gly Asn Ser Thr Asn
        435                 440                 445
Ala Thr Pro Tyr Thr Asn Ala Val Gly Phe Met Pro Asn Leu Ala Ala
    450                 455                 460
Tyr Pro Lys Thr Gln Ser Gln Thr Ala Lys Asn Asn Ile Val Ser Gln
465                 470                 475                 480
Val Tyr Leu Asn Gly Asp Lys Ser Lys Pro Met Ile Leu Thr Ile Thr
                485                 490                 495
Leu Asn Gly Thr Asn Glu Ser Ser Glu Thr Ser Gln Val Ser His Tyr
            500                 505                 510
Ser Met Ser Phe Thr Trp Ala Trp Glu Ser Gly Gln Tyr Ala Thr Glu
        515                 520                 525
Thr Phe Ala Thr Asn Ser Phe Thr Phe Ser Tyr Ile Ala Glu Gln
    530                 535                 540
```

<210> 64
<211> 1335
<212> DNA
<213> Chimpanzee Adenovirus- ChAd 26 Fiber

<400> 64
atgtccaaaa agcgcgtccg ggtggatgat gacttcgacc ccgtctaccc ctacgatgca 60
gacaacgcac cgaccgtgcc cttcatcaac ccccccttcg tctcttcaga tggattccaa 120
gagaagcccc tgggggtgct gtccctgcgt ctggccgatc ccgtcaccac caagaacggg 180
gaaatcaccc tcaagctggg agatggggtg gacctcgacg actcgggaaa actcatctcc 240
aacacggcca ccaaggccgc cgcccctctc agtttttcca acaacaccat ttcccttaac 300
atggataccc ctctttacaa caacaatgga aagctaggta tgaaggtaac cgcaccatta 360
aagatattag acacagatct actaaaaaca cttgttgttg cttatgggca gggattagga 420
acaaacacca atggtgctct tgttgcccaa ctagcatacc cacttgtttt taataccgct 480
agcaaaattg cccttaattt aggcaatgga ccattaaaag tggatgcaaa tagactgaac 540
attaattgca aaagaggtat ctatgtcact accacaaaag atgcactgga gattaatatc 600
agttgggcaa atgctatgac atttatagga aatgccattg gtgtcaatat tgacacaaaa 660

```
aaaggcctac agttcggcac ttcaagcact gaaacagatg ttaaaaatgc ttttccactc 720
caagtaaaac ttggagctgg tcttacattt gacagcacag gtgccattgt tgcttggaac 780
aaagaagatg acaaacttac actgtggacc acagccgatc catctccaaa ctgtcacata 840
tattctgcaa aggatgctaa gcttacactc tgcttgacaa agtgtggtag tcaaatccta 900
ggcactgtct ccctattagc agtcagtggc agcttggctc ctatcacagg ggctgttaga 960
actgcacttg tatcactcaa attcaatgct aatggagccc ttttggacaa atcaactctg 1020
aacaaagaat actggaacta cagacaagga gatctaattc caggtacacc atatacacat 1080
gctgtgggtt tcatgcctaa caaaaaagcc taccctaaaa acacaactgc agcttccaag 1140
agccacattg tgggtgatgt gtatttagat ggagatgcag ataaaccttt atctcttatc 1200
atcactttca atgaaactga tgatgaaacc tgtgattact gcatcaactt tcaatggaaa 1260
tggggagctg atcaatataa ggataagaca ctcgcaacca gttcattcac cttctcatac 1320
atcgcccaag aataa                                                  1335

<210> 65
<211> 444
<212> PRT
<213> Chimpanzee Adenovirus- ChAd 26 Fiber

<400> 65
Met Ser Lys Lys Arg Val Arg Val Asp Asp Asp Phe Asp Pro Val Tyr
 1               5                  10                  15
Pro Tyr Asp Ala Asp Asn Ala Pro Thr Val Pro Phe Ile Asn Pro Pro
            20                  25                  30
Phe Val Ser Ser Asp Gly Phe Gln Glu Lys Pro Leu Gly Val Leu Ser
        35                  40                  45
Leu Arg Leu Ala Asp Pro Val Thr Thr Lys Asn Gly Glu Ile Thr Leu
    50                  55                  60
Lys Leu Gly Asp Gly Val Asp Leu Asp Asp Ser Gly Lys Leu Ile Ser
65                  70                  75                  80
Asn Thr Ala Thr Lys Ala Ala Ala Pro Leu Ser Phe Ser Asn Asn Thr
                85                  90                  95
Ile Ser Leu Asn Met Asp Thr Pro Leu Tyr Asn Asn Asn Gly Lys Leu
            100                 105                 110
Gly Met Lys Val Thr Ala Pro Leu Lys Ile Leu Asp Thr Asp Leu Leu
        115                 120                 125
Lys Thr Leu Val Val Ala Tyr Gly Gln Gly Leu Gly Thr Asn Thr Asn
    130                 135                 140
Gly Ala Leu Val Ala Gln Leu Ala Tyr Pro Leu Val Phe Asn Thr Ala
145                 150                 155                 160
Ser Lys Ile Ala Leu Asn Leu Gly Asn Gly Pro Leu Lys Val Asp Ala
                165                 170                 175
Asn Arg Leu Asn Ile Asn Cys Lys Arg Gly Ile Tyr Val Thr Thr Thr
            180                 185                 190
Lys Asp Ala Leu Glu Ile Asn Ile Ser Trp Ala Asn Ala Met Thr Phe
        195                 200                 205
Ile Gly Asn Ala Ile Gly Val Asn Ile Asp Thr Lys Lys Gly Leu Gln
    210                 215                 220
Phe Gly Thr Ser Ser Thr Glu Thr Asp Val Lys Asn Ala Phe Pro Leu
225                 230                 235                 240
Gln Val Lys Leu Gly Ala Gly Leu Thr Phe Asp Ser Thr Gly Ala Ile
                245                 250                 255
Val Ala Trp Asn Lys Glu Asp Asp Lys Leu Thr Leu Trp Thr Thr Ala
            260                 265                 270
Asp Pro Ser Pro Asn Cys His Ile Tyr Ser Ala Lys Asp Ala Lys Leu
        275                 280                 285
```

```
Thr Leu Cys Leu Thr Lys Cys Gly Ser Gln Ile Leu Gly Thr Val Ser
    290                 295                 300
Leu Leu Ala Val Ser Gly Ser Leu Ala Pro Ile Thr Gly Ala Val Arg
305                 310                 315                 320
Thr Ala Leu Val Ser Leu Lys Phe Asn Ala Asn Gly Ala Leu Leu Asp
                325                 330                 335
Lys Ser Thr Leu Asn Lys Glu Tyr Trp Asn Tyr Arg Gln Gly Asp Leu
            340                 345                 350
Ile Pro Gly Thr Pro Tyr Thr His Ala Val Gly Phe Met Pro Asn Lys
        355                 360                 365
Lys Ala Tyr Pro Lys Asn Thr Thr Ala Ala Ser Lys Ser His Ile Val
    370                 375                 380
Gly Asp Val Tyr Leu Asp Gly Asp Ala Asp Lys Pro Leu Ser Leu Ile
385                 390                 395                 400
Ile Thr Phe Asn Glu Thr Asp Asp Glu Thr Cys Asp Tyr Cys Ile Asn
                405                 410                 415
Phe Gln Trp Lys Trp Gly Ala Asp Gln Tyr Lys Asp Lys Thr Leu Ala
            420                 425                 430
Thr Ser Ser Phe Thr Phe Ser Tyr Ile Ala Gln Glu
        435                 440
```

<210> 66
<211> 1062
<212> DNA
<213> Chimpanzee Adenovirus- ChAd 30 Fiber

<400> 66
```
atggccaaac gagctcggct aagcagctcc ttcaatccgg tctaccccta tgaagatgaa 60
agcagctcac aacacccctt tataaaccct ggtttcattt cctcaaatgg ttttgcacaa 120
agcccagatg gagttctaac tcttaaatgt gttaatccgc tcactaccgc cagcggaccc 180
ctccaactta aagttggaag cagtcttaca gtagatacta tcgatgggtc tttggaggaa 240
aatataactg ccgcagcgcc actcactaaa actaaccact ccataggttt atcaatagga 300
tctggcttgc aaacaaagga tgataaactt tgtttatcgc tgggagatgg gttggtaaca 360
aaggatgata aactatgttt atcgctggga gatgggttaa taacaaaaga tgatacacta 420
tgtgccaaac taggacatgg ccttgtgttt gactcttcca atgctatcac catagaaaac 480
aacaccttgt ggacaggtgc aaaaccaagc gccaactgtg taattaaaga gggagaagat 540
tccccagact gtaagctcac tttagttcta gtgaagaatg gaggactgat aaatggatac 600
ataacattaa tgggagcctc agaatatact aacaccttgt ttaaaaacaa acaagttaca 660
atcgatgtaa acctcgcatt tgataatact ggccaaatta tcacttacct atcatccctt 720
aaaagtaacc tgaactttaa agacaaccaa aacatggcta ctggaaccat aaccagtgcc 780
aaaggcttca tgcccagcac caccgcctat ccatttataa catacgccac tcagtcccta 840
aatgaagatt acatttatgg agagtgttac tacaaatcta ccaatggaac tctctttcca 900
ctaaaagtta ctgtcacact aaacagacgt atgtcagctt ctggaatggc ctatgctatg 960
aatttttcat ggtctctaaa tgcagaggaa gccccggaaa ctaccgaagt cactctcatt 1020
acctcccccc tctttttttc ttatatcaga gaagatgact ga                    1062
```

<210> 67
<211> 353
<212> PRT
<213> Chimpanzee Adenovirus- ChAd 30 Fiber

<400> 67
```
Met Ala Lys Arg Ala Arg Leu Ser Ser Ser Phe Asn Pro Val Tyr Pro
 1               5                  10                  15
```

```
Tyr Glu Asp Glu Ser Ser Ser Gln His Pro Phe Ile Asn Pro Gly Phe
            20                  25                  30
Ile Ser Ser Asn Gly Phe Ala Gln Ser Pro Asp Gly Val Leu Thr Leu
        35                  40                  45
Lys Cys Val Asn Pro Leu Thr Thr Ala Ser Gly Pro Leu Gln Leu Lys
    50                  55                  60
Val Gly Ser Ser Leu Thr Val Asp Thr Ile Asp Gly Ser Leu Glu Glu
65                  70                  75                  80
Asn Ile Thr Ala Ala Ala Pro Leu Thr Lys Thr Asn His Ser Ile Gly
                85                  90                  95
Leu Ser Ile Gly Ser Gly Leu Gln Thr Lys Asp Asp Lys Leu Cys Leu
            100                 105                 110
Ser Leu Gly Asp Gly Leu Val Thr Lys Asp Asp Lys Leu Cys Leu Ser
        115                 120                 125
Leu Gly Asp Gly Leu Ile Thr Lys Asp Asp Thr Leu Cys Ala Lys Leu
    130                 135                 140
Gly His Gly Leu Val Phe Asp Ser Ser Asn Ala Ile Thr Ile Glu Asn
145                 150                 155                 160
Asn Thr Leu Trp Thr Gly Ala Lys Pro Ser Ala Asn Cys Val Ile Lys
                165                 170                 175
Glu Gly Glu Asp Ser Pro Asp Cys Lys Leu Thr Leu Val Leu Val Lys
            180                 185                 190
Asn Gly Gly Leu Ile Asn Gly Tyr Ile Thr Leu Met Gly Ala Ser Glu
        195                 200                 205
Tyr Thr Asn Thr Leu Phe Lys Asn Lys Gln Val Thr Ile Asp Val Asn
    210                 215                 220
Leu Ala Phe Asp Asn Thr Gly Gln Ile Ile Thr Tyr Leu Ser Ser Leu
225                 230                 235                 240
Lys Ser Asn Leu Asn Phe Lys Asp Asn Gln Asn Met Ala Thr Gly Thr
                245                 250                 255
Ile Thr Ser Ala Lys Gly Phe Met Pro Ser Thr Thr Ala Tyr Pro Phe
            260                 265                 270
Ile Thr Tyr Ala Thr Gln Ser Leu Asn Glu Asp Tyr Ile Tyr Gly Glu
        275                 280                 285
Cys Tyr Tyr Lys Ser Thr Asn Gly Thr Leu Phe Pro Leu Lys Val Thr
    290                 295                 300
Val Thr Leu Asn Arg Arg Met Ser Ala Ser Gly Met Ala Tyr Ala Met
305                 310                 315                 320
Asn Phe Ser Trp Ser Leu Asn Ala Glu Glu Ala Pro Glu Thr Thr Glu
                325                 330                 335
Val Thr Leu Ile Thr Ser Pro Phe Phe Phe Ser Tyr Ile Arg Glu Asp
            340                 345                 350
Asp
```

<210> 68
<211> 1791
<212> DNA
<213> Chimpanzee Adenovirus- ChAd 31 Fiber

<400> 68
atgtcagatt cttgctcctg tccctccgca cccactatct tcatgttgtt gcagatgaag 60
cgcaccaaaa cgtctgacga gagcttcaac cccgtgtacc cctatgacac ggaaagcggc 120
cctccctccg tccctttcct cacccctccc ttcgtgtctc ccgatggatt ccaagaaagt 180

```
ccccccgggg tcctgtctct gaacctggcc gagcccctgg tcacttccca cggcatgctc 240
gccctgaaaa tgggaagtgg cctctccctg gacgacgctg gcaacctcac ctctcaagat 300
atcaccaccg ctagccctcc cctcaaaaaa accaagacca acctcagcct agaaacctca 360
tccccctaa ctgtgagcac ctcaggcgcc ctcaccgtag cagccgccgc tcccctggcg 420
gtggccggca cctccctcac catgcaatca gaggcccccc tgacagtaca ggatgcaaaa 480
ctcaccctgg ccaccaaagg ccccctgacc gtgtctgaag gcaaactggc cttgcaaaca 540
tcggccccgc tgacggccgc tgacagcagc accctcacag tcagtgccac accacccctt 600
agcacaagca atggcagctt gggtattgac atgcaagccc ccatttacac caccaatgga 660
aaactaggac ttaactttgg cgctcccctg catgtggtag acagcctaaa tgcactgact 720
gtagttactg gccaaggtct tacgataaac ggaacagccc tacaaactag agtctcaggt 780
gccctcaact atgacacatc aggaaaccta gaattgagag ctgcaggggg tatgcgagtt 840
gatgcaaatg gtcaacttat ccttgatgta gcttacccat ttgatgcaca aaacaatctc 900
agccttaggc ttggacaggg acccctgttt gttaactctg cccacaactt ggatgttaac 960
tacaacagag gcctctacct gttcacatct ggaaatacca aaaagctaga agttaatatc 1020
aaaacagcca agggtctcat ttatgatgac actgctatag caatcaatgc gggtgatggg 1080
ctacagtttg actcaggctc agatacaaat ccattaaaaa ctaaacttgg attaggactg 1140
gattatgact ccagcagagc cataattgct aaactgggaa ctggcctaag ctttgacaac 1200
acaggtgcca tcacagtagg caacaaaaat gatgacaagc ttaccttgtg gaccacacca 1260
gacccatccc ctaactgtag aatctattca gagaaagatg ctaaattcac acttgttttg 1320
actaaatgcg gcagtcaggt gttggccagc gtttctgttt tatctgtaaa aggtagcctt 1380
gcgcccatca gtggcacagt aactagtgct cagattgtcc tcagatttga tgaaaatgga 1440
gttctactaa gcaattcttc ccttgaccct caatactgga actacagaaa aggtgacctt 1500
acagagggca ctgcatatac caacgcagtg ggatttatgc ccaacctcac agcataccca 1560
aaaacacaga gccaaactgc taaaagcaac attgtaagtc aggtttactt gaatggggac 1620
aaatccaaac ccatgaccct caccattacc ctcaatggaa ctaatgaaac aggagatgcc 1680
acagtaagca cttactccat gtcattctca tggaactgga atggaagtaa ttacattaat 1740
gaaacgttcc aaaccaactc cttcaccttc tcctacatcg cccaagaata a           1791
```

<210> 69
<211> 578
<212> PRT
<213> Chimpanzee Adenovirus- ChAd 31 Fiber

<400> 69

```
Met Lys Arg Thr Lys Thr Ser Asp Glu Ser Phe Asn Pro Val Tyr Pro
 1               5                  10                  15
Tyr Asp Thr Glu Ser Gly Pro Pro Ser Val Pro Phe Leu Thr Pro Pro
            20                  25                  30
Phe Val Ser Pro Asp Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser
        35                  40                  45
Leu Asn Leu Ala Glu Pro Leu Val Thr Ser His Gly Met Leu Ala Leu
    50                  55                  60
Lys Met Gly Ser Gly Leu Ser Leu Asp Asp Ala Gly Asn Leu Thr Ser
65                  70                  75                  80
Gln Asp Ile Thr Thr Ala Ser Pro Pro Leu Lys Lys Thr Lys Thr Asn
                85                  90                  95
Leu Ser Leu Glu Thr Ser Ser Pro Leu Thr Val Ser Thr Ser Gly Ala
            100                 105                 110
Leu Thr Val Ala Ala Ala Ala Pro Leu Ala Val Ala Gly Thr Ser Leu
        115                 120                 125
Thr Met Gln Ser Glu Ala Pro Leu Thr Val Gln Asp Ala Lys Leu Thr
    130                 135                 140
Leu Ala Thr Lys Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu
145                 150                 155                 160
Gln Thr Ser Ala Pro Leu Thr Ala Ala Asp Ser Ser Thr Leu Thr Val
```

```
                 165                 170                 175
Ser Ala Thr Pro Pro Leu Ser Thr Ser Asn Gly Ser Leu Gly Ile Asp
             180                 185                 190
Met Gln Ala Pro Ile Tyr Thr Thr Asn Gly Lys Leu Gly Leu Asn Phe
         195                 200                 205
Gly Ala Pro Leu His Val Val Asp Ser Leu Asn Ala Leu Thr Val Val
     210                 215                 220
Thr Gly Gln Gly Leu Thr Ile Asn Gly Thr Ala Leu Gln Thr Arg Val
225                 230                 235                 240
Ser Gly Ala Leu Asn Tyr Asp Thr Ser Gly Asn Leu Glu Leu Arg Ala
                245                 250                 255
Ala Gly Gly Met Arg Val Asp Ala Asn Gly Gln Leu Ile Leu Asp Val
            260                 265                 270
Ala Tyr Pro Phe Asp Ala Gln Asn Asn Leu Ser Leu Arg Leu Gly Gln
        275                 280                 285
Gly Pro Leu Phe Val Asn Ser Ala His Asn Leu Asp Val Asn Tyr Asn
    290                 295                 300
Arg Gly Leu Tyr Leu Phe Thr Ser Gly Asn Thr Lys Lys Leu Glu Val
305                 310                 315                 320
Asn Ile Lys Thr Ala Lys Gly Leu Ile Tyr Asp Asp Thr Ala Ile Ala
                325                 330                 335
Ile Asn Ala Gly Asp Gly Leu Gln Phe Asp Ser Gly Ser Asp Thr Asn
            340                 345                 350
Pro Leu Lys Thr Lys Leu Gly Leu Gly Leu Asp Tyr Asp Ser Ser Arg
        355                 360                 365
Ala Ile Ile Ala Lys Leu Gly Thr Gly Leu Ser Phe Asp Asn Thr Gly
    370                 375                 380
Ala Ile Thr Val Gly Asn Lys Asn Asp Asp Lys Leu Thr Leu Trp Thr
385                 390                 395                 400
Thr Pro Asp Pro Ser Pro Asn Cys Arg Ile Tyr Ser Glu Lys Asp Ala
                405                 410                 415
Lys Phe Thr Leu Val Leu Thr Lys Cys Gly Ser Gln Val Leu Ala Ser
            420                 425                 430
Val Ser Val Leu Ser Val Lys Gly Ser Leu Ala Pro Ile Ser Gly Thr
        435                 440                 445
Val Thr Ser Ala Gln Ile Val Leu Arg Phe Asp Glu Asn Gly Val Leu
    450                 455                 460
Leu Ser Asn Ser Ser Leu Asp Pro Gln Tyr Trp Asn Tyr Arg Lys Gly
465                 470                 475                 480
Asp Leu Thr Glu Gly Thr Ala Tyr Thr Asn Ala Val Gly Phe Met Pro
                485                 490                 495
Asn Leu Thr Ala Tyr Pro Lys Thr Gln Ser Gln Thr Ala Lys Ser Asn
            500                 505                 510
Ile Val Ser Gln Val Tyr Leu Asn Gly Asp Lys Ser Lys Pro Met Thr
        515                 520                 525
Leu Thr Ile Thr Leu Asn Gly Thr Asn Glu Thr Gly Asp Ala Thr Val
    530                 535                 540
Ser Thr Tyr Ser Met Ser Phe Ser Trp Asn Trp Asn Gly Ser Asn Tyr
545                 550                 555                 560
Ile Asn Glu Thr Phe Gln Thr Asn Ser Phe Thr Phe Ser Tyr Ile Ala
                565                 570                 575
Gln Glu
```

<210> 70
<211> 978
<212> DNA
<213> Chimpanzee Adenovirus- ChAd 37 Fiber

<400> 70
atggccaaac gggctcgtct aagcagctcc ttcaacccgg tgtaccccta tgaagacgag 60
agcagctcac aacacccatt tataaacccc ggcttcattt cccctgatgg ctttacacaa 120
agcccagacg gagttctaac actgaaatgt gtttcccctc ttactaccac cagtggcgct 180
ctagacatta aagtgggaag agggcttaaa gtagatagca ctgatggttc cctggaagaa 240
aatatagaca ttacagctcc cctcactaaa tttaaccact cagtaggatt agcatttggc 300
gacggtctag aaacaaaaga aaacaagctt tatgtaaaac ttggagatgg acttaaattt 360
agctctggca gtatatacat tgaccatgat gttaacactt tatggacagg agtcaatcca 420
agtgctaact gtataattac agacaatgga gaaaccaatg acagcaagct taccctaata 480
cttgttaagt caggtggatt aataaatgct tatgtctcat taatgggtga ctcagacaca 540
gtcaataaat taaccacaga aaaaagtgct caaattaccg ttgacatata ctttgataat 600
caaggaaaag ttcttactga actatcggcc cttaaaacag atcttaaaca taaatttggt 660
caaaacatgg cttctagcga agtatcaaac tgcaaaggct ttatgccaag cttaaatgca 720
tacccattca gaaatccaac taaacctacc aaaggaagag aagactacat ttatggaata 780
acttactatc aagccacaga tggtaatctc tatgagctaa aaactactat tactctaaac 840
cacagtgtca ttagttctct atgtgcatat gcaatgcaca tttcatggtc atgggacacc 900
gtaacagagc cagagacaac acccactact cttattacct ccccccttctc cttttcctat 960
atcagagaag atgactga 978

<210> 71
<211> 325
<212> PRT
<213> Chimpanzee Adenovirus- ChAd 37 Fiber

<400> 71
Met Ala Lys Arg Ala Arg Leu Ser Ser Ser Phe Asn Pro Val Tyr Pro
 1   5   10   15
Tyr Glu Asp Glu Ser Ser Ser Gln His Pro Phe Ile Asn Pro Gly Phe
            20   25   30
Ile Ser Pro Asp Gly Phe Thr Gln Ser Pro Asp Gly Val Leu Thr Leu
        35   40   45
Lys Cys Val Ser Pro Leu Thr Thr Thr Ser Gly Ala Leu Asp Ile Lys
    50   55   60
Val Gly Arg Gly Leu Lys Val Asp Ser Thr Asp Gly Ser Leu Glu Glu
65   70   75   80
Asn Ile Asp Ile Thr Ala Pro Leu Thr Lys Phe Asn His Ser Val Gly
                85   90   95
Leu Ala Phe Gly Asp Gly Leu Glu Thr Lys Glu Asn Lys Leu Tyr Val
            100   105   110
Lys Leu Gly Asp Gly Leu Lys Phe Ser Ser Gly Ser Ile Tyr Ile Asp
        115   120   125
His Asp Val Asn Thr Leu Trp Thr Gly Val Asn Pro Ser Ala Asn Cys
    130   135   140
Ile Ile Thr Asp Asn Gly Glu Thr Asn Asp Ser Lys Leu Thr Leu Ile
145   150   155   160
Leu Val Lys Ser Gly Gly Leu Ile Asn Ala Tyr Val Ser Leu Met Gly
                165   170   175
Asp Ser Asp Thr Val Asn Lys Leu Thr Thr Glu Lys Ser Ala Gln Ile
            180   185   190
Thr Val Asp Ile Tyr Phe Asp Asn Gln Gly Lys Val Leu Thr Glu Leu

```
        195                 200                 205
Ser Ala Leu Lys Thr Asp Leu Lys His Lys Phe Gly Gln Asn Met Ala
    210                 215                 220
Ser Ser Glu Val Ser Asn Cys Lys Gly Phe Met Pro Ser Leu Asn Ala
225                 230                 235                 240
Tyr Pro Phe Arg Asn Pro Thr Lys Pro Thr Lys Gly Arg Glu Asp Tyr
                245                 250                 255
Ile Tyr Gly Ile Thr Tyr Tyr Gln Ala Thr Asp Gly Asn Leu Tyr Glu
            260                 265                 270
Leu Lys Thr Thr Ile Thr Leu Asn His Ser Val Ile Ser Ser Leu Cys
        275                 280                 285
Ala Tyr Ala Met His Ile Ser Trp Ser Trp Asp Thr Val Thr Glu Pro
    290                 295                 300
Glu Thr Thr Pro Thr Thr Leu Ile Thr Ser Pro Phe Ser Phe Ser Tyr
305                 310                 315                 320
Ile Arg Glu Asp Asp
                325
```

<210> 72
<211> 1332
<212> DNA
<213> Chimpanzee Adenovirus- ChAd 38 Fiber

<400> 72

```
atgtccaaaa agcgcgtccg ggtggatgat gacttcgacc ccgtctaccc ctacgatgca 60
gacaacgcac cgaccgtgcc cttcatcaac ccccccttcg tctcttcaga tggattccaa 120
gagaagcccc tgggggtgtt gtccctgcga ctggccgacc ccgtcaccac caagaacggg 180
gaaatcaccc tcaagctggg agagggggtg gacctcgact cctcgggaaa actcatctcc 240
aacacggcca ccaaggccgc cgcccctctc agtttttcca acaacaccat ttcccttaac 300
atggataccc ctttttatac caaagatgga aaattatcct tacaagtttc tccaccatta 360
aacatattaa aatcaaccat tctgaacaca ttagctgtag cttatggatc aggtttagga 420
ctcagtggtg gcactgctct tgcagtacag ttggcctctc cactcacctt tgatgaaaaa 480
ggaaatatta aaattaacct agccagtggt ccattaacag ttgatgcaag tcgacttagt 540
atcaactgca aaagaggggt cactgtcact accgcaggag atgcaattaa aagcaacata 600
agctggccta aaggtataag atttgaaggt gatgccatag ctgcaaacat tggcagagga 660
ttggaatttg gaaccactag tacagagact gatgtcacag atgcataccc aattcaagtt 720
aaattgggta ctggtctcac ctttgacagt acaggcgcca ttgttgcatg gaacaaagag 780
gatgataaac ttacattatg gaccacagcc gacccctcgc caaattgcaa aatatactct 840
gaaaaagatg ctaaactcac actttgcttg acaaaatgtg gaagccaaat tctgggcact 900
gtgactgtat tggcagtgaa taatggaagt ctcaacccaa tcacaaacac agtaagcact 960
gcacttgtct ccctcaagtt tgatgcaagt ggagttttgc taagcagctc cacattagac 1020
aaagaatatt ggaacttccg aaagggagat gttacacctg ctgaacccta tactaatgct 1080
ataggtttta tgcctaacat aaaggcctat cctaaaaaca catctgcagc ttcaaaaagc 1140
catattgtca gtcaagttta tctcaatggg gatgaaacca aacctctgat gctgattatt 1200
acttttaatg aaactgagga tgcaacttgc acctatagta tcacttttca atggaaatgg 1260
gatagtacta agtacacagg taaaacactt gctaccagct ccttcacctt ctcctacatt 1320
gctcaagaat ga                                                    1332
```

<210> 73
<211> 443
<212> PRT
<213> Chimpanzee Adenovirus- ChAd 38 Fiber

<400> 73

```
Met Ser Lys Lys Arg Val Arg Val Asp Asp Asp Phe Asp Pro Val Tyr
 1               5                  10                  15
Pro Tyr Asp Ala Asp Asn Ala Pro Thr Val Pro Phe Ile Asn Pro Pro
            20                  25                  30
Phe Val Ser Ser Asp Gly Phe Gln Glu Lys Pro Leu Gly Val Leu Ser
        35                  40                  45
Leu Arg Leu Ala Asp Pro Val Thr Thr Lys Asn Gly Glu Ile Thr Leu
    50                  55                  60
Lys Leu Gly Glu Gly Val Asp Leu Asp Ser Ser Gly Lys Leu Ile Ser
65                  70                  75                  80
Asn Thr Ala Thr Lys Ala Ala Ala Pro Leu Ser Phe Ser Asn Asn Thr
                85                  90                  95
Ile Ser Leu Asn Met Asp Thr Pro Phe Tyr Thr Lys Asp Gly Lys Leu
            100                 105                 110
Ser Leu Gln Val Ser Pro Pro Leu Asn Ile Leu Lys Ser Thr Ile Leu
        115                 120                 125
Asn Thr Leu Ala Val Ala Tyr Gly Ser Gly Leu Gly Leu Ser Gly Gly
    130                 135                 140
Thr Ala Leu Ala Val Gln Leu Ala Ser Pro Leu Thr Phe Asp Glu Lys
145                 150                 155                 160
Gly Asn Ile Lys Ile Asn Leu Ala Ser Gly Pro Leu Thr Val Asp Ala
                165                 170                 175
Ser Arg Leu Ser Ile Asn Cys Lys Arg Gly Val Thr Val Thr Thr Ala
            180                 185                 190
Gly Asp Ala Ile Lys Ser Asn Ile Ser Trp Pro Lys Gly Ile Arg Phe
        195                 200                 205
Glu Gly Asp Ala Ile Ala Ala Asn Ile Gly Arg Gly Leu Glu Phe Gly
    210                 215                 220
Thr Thr Ser Thr Glu Thr Asp Val Thr Asp Ala Tyr Pro Ile Gln Val
225                 230                 235                 240
Lys Leu Gly Thr Gly Leu Thr Phe Asp Ser Thr Gly Ala Ile Val Ala
                245                 250                 255
Trp Asn Lys Glu Asp Asp Lys Leu Thr Leu Trp Thr Thr Ala Asp Pro
            260                 265                 270
Ser Pro Asn Cys Lys Ile Tyr Ser Glu Lys Asp Ala Lys Leu Thr Leu
        275                 280                 285
Cys Leu Thr Lys Cys Gly Ser Gln Ile Leu Gly Thr Val Thr Val Leu
    290                 295                 300
Ala Val Asn Asn Gly Ser Leu Asn Pro Ile Thr Asn Thr Val Ser Thr
305                 310                 315                 320
Ala Leu Val Ser Leu Lys Phe Asp Ala Ser Gly Val Leu Leu Ser Ser
                325                 330                 335
Ser Thr Leu Asp Lys Glu Tyr Trp Asn Phe Arg Lys Gly Asp Val Thr
            340                 345                 350
Pro Ala Glu Pro Tyr Thr Asn Ala Ile Gly Phe Met Pro Asn Ile Lys
        355                 360                 365
Ala Tyr Pro Lys Asn Thr Ser Ala Ala Ser Lys Ser His Ile Val Ser
    370                 375                 380
Gln Val Tyr Leu Asn Gly Asp Glu Thr Lys Pro Leu Met Leu Ile Ile
385                 390                 395                 400
Thr Phe Asn Glu Thr Glu Asp Ala Thr Cys Thr Tyr Ser Ile Thr Phe
                405                 410                 415
Gln Trp Lys Trp Asp Ser Thr Lys Tyr Thr Gly Lys Thr Leu Ala Thr
            420                 425                 430
Ser Ser Phe Thr Phe Ser Tyr Ile Ala Gln Glu
```

435 440

<210> 74
<211> 1332
<212> DNA
<213> Chimpanzee Adenovirus- ChAd 44 Fiber

<400> 74
atgtccaaaa agcgcgtccg ggtggatgat gacttcgacc ccgtctaccc ctacgatgca 60
gacaacgcac cgaccgtgcc cttcatcaac ccccccttcg tctcttcaga tggattccaa 120
gagaagcccc tgggggtgtt gtccctgcga ctggctgacc ccgtcaccac caagaacggg 180
gaaatcaccc tcaagctggg agaggggtg gacctcgact cgtcgggaaa actcatctcc 240
aacacggcca ccaaggccgc cgcccctctc agtatttcaa acaacaccat ttcccttaaa 300
actgctgccc ctttctacaa caacaatgga actttaagcc tcaatgtctc cacaccatta 360
gcagtatttc ccacatttaa cactttaggc ataagtcttg gaaacggtct tcagacttca 420
aataagttgt tgactgtaca actaactcat cctcttacat tcagctcaaa tagcatcaca 480
gtaaaaacag acaaagggct atatattaac tccagtggaa acagaggact tgaggctaat 540
ataagcctaa aaagaggact agtttttgac ggtaatgcta ttgcaacata tattggaaat 600
ggcttagact atggatctta tgatagtgat ggaaaaacaa gacccgtaat taccaaaatt 660
ggagcaggat taaattttga tgctaacaaa gcaatagctg tcaaactagg cacaggttta 720
agttttgact ccgctggtgc cttgacagct ggaaacaaac aggatgacaa gctaacactt 780
tggactaccc ctgacccaag ccctaattgt caattacttt cagacagaga tgccaaattt 840
actctctgtc ttacaaaatg cggtagtcaa atactaggca ctgtggcagt ggcggctgtt 900
actgtaggat cagcactaaa tccaattaat gacacagtca aaagcgccat agttttcctt 960
agatttgatt ccgatggtgt actcatgtca aactcatcaa tggtaggtga ttactggaac 1020
tttagggagg gacagaccac tcaaagtgta gcctatacaa atgctgtggg attcatgcca 1080
aatataggtg catatccaaa aacccaaagt aaaacaccta aaaatagcat agtcagtcag 1140
gtatatttaa ctggagaaac tactatgcca atgacactaa ccataacttt caatggcact 1200
gatgaaaaag acacaacccc agttagcacc tactctatga cttttacatg gcagtggact 1260
ggagactata aggacaaaaa tattaccttt gctaccaact cattctcttt ttcctacatc 1320
gcccaggaat aa 1332

<210> 75
<211> 443
<212> PRT
<213> Chimpanzee Adenovirus- ChAd 44 Fiber

<400> 75
Met Ser Lys Lys Arg Val Arg Val Asp Asp Asp Phe Asp Pro Val Tyr
1 5 10 15
Pro Tyr Asp Ala Asp Asn Ala Pro Thr Val Pro Phe Ile Asn Pro Pro
20 25 30
Phe Val Ser Ser Asp Gly Phe Gln Glu Lys Pro Leu Gly Val Leu Ser
35 40 45
Leu Arg Leu Ala Asp Pro Val Thr Thr Lys Asn Gly Glu Ile Thr Leu
50 55 60
Lys Leu Gly Glu Gly Val Asp Leu Asp Ser Ser Gly Lys Leu Ile Ser
65 70 75 80
Asn Thr Ala Thr Lys Ala Ala Ala Pro Leu Ser Ile Ser Asn Asn Thr
85 90 95
Ile Ser Leu Lys Thr Ala Ala Pro Phe Tyr Asn Asn Asn Gly Thr Leu
100 105 110
Ser Leu Asn Val Ser Thr Pro Leu Ala Val Phe Pro Thr Phe Asn Thr
115 120 125

```
Leu Gly Ile Ser Leu Gly Asn Gly Leu Gln Thr Ser Asn Lys Leu Leu
    130                 135                 140
Thr Val Gln Leu Thr His Pro Leu Thr Phe Ser Ser Asn Ser Ile Thr
145                 150                 155                 160
Val Lys Thr Asp Lys Gly Leu Tyr Ile Asn Ser Ser Gly Asn Arg Gly
                165                 170                 175
Leu Glu Ala Asn Ile Ser Leu Lys Arg Gly Leu Val Phe Asp Gly Asn
            180                 185                 190
Ala Ile Ala Thr Tyr Ile Gly Asn Gly Leu Asp Tyr Gly Ser Tyr Asp
        195                 200                 205
Ser Asp Gly Lys Thr Arg Pro Val Ile Thr Lys Ile Gly Ala Gly Leu
    210                 215                 220
Asn Phe Asp Ala Asn Lys Ala Ile Ala Val Lys Leu Gly Thr Gly Leu
225                 230                 235                 240
Ser Phe Asp Ser Ala Gly Ala Leu Thr Ala Gly Asn Lys Gln Asp Asp
                245                 250                 255
Lys Leu Thr Leu Trp Thr Thr Pro Asp Pro Ser Pro Asn Cys Gln Leu
            260                 265                 270
Leu Ser Asp Arg Asp Ala Lys Phe Thr Leu Cys Leu Thr Lys Cys Gly
        275                 280                 285
Ser Gln Ile Leu Gly Thr Val Ala Val Ala Ala Val Thr Val Gly Ser
    290                 295                 300
Ala Leu Asn Pro Ile Asn Asp Thr Val Lys Ser Ala Ile Val Phe Leu
305                 310                 315                 320
Arg Phe Asp Ser Asp Gly Val Leu Met Ser Asn Ser Ser Met Val Gly
                325                 330                 335
Asp Tyr Trp Asn Phe Arg Glu Gly Gln Thr Thr Gln Ser Val Ala Tyr
            340                 345                 350
Thr Asn Ala Val Gly Phe Met Pro Asn Ile Gly Ala Tyr Pro Lys Thr
        355                 360                 365
Gln Ser Lys Thr Pro Lys Asn Ser Ile Val Ser Gln Val Tyr Leu Thr
    370                 375                 380
Gly Glu Thr Thr Met Pro Met Thr Leu Thr Ile Thr Phe Asn Gly Thr
385                 390                 395                 400
Asp Glu Lys Asp Thr Thr Pro Val Ser Thr Tyr Ser Met Thr Phe Thr
                405                 410                 415
Trp Gln Trp Thr Gly Asp Tyr Lys Asp Lys Asn Ile Thr Phe Ala Thr
            420                 425                 430
Asn Ser Phe Ser Phe Ser Tyr Ile Ala Gln Glu
        435                 440
```

<210> 76
<211> 1278
<212> DNA
<213> Chimpanzee Adenovirus- ChAd 63 Fiber

<400> 76
atgtccaaaa agcgcgtccg ggtggatgat gacttcgacc ccgtctaccc ctacgatgca 60
gacaacgcac cgaccgtgcc cttcatcaac ccccccttcg tctcttcaga tggattccaa 120
gagaagcccc tgggggtgct gtccctgcga ctggccgacc ccgtcaccac caagaacggg 180
gaaatcaccc tcaagctggg agagggggtg gacctcgact cctcgggaaa actcatctcc 240
aacacggcca ccaaggccgc cgcccctctc agtttttcca acaacaccat ttcccttaac 300
atggatcacc ccttttacac taaagatgga aaattatcct tacaagtttc tccaccatta 360
aatatactga gaacaagcat tctaaacaca ctagctttag gttttggatc aggtttagga 420

```
ctccgtggct ctgccttggc agtacagtta gtctctccac ttacatttga tactgatgga 480
aacataaagc ttaccttaga cagaggtttg catgttacaa caggagatgc aattgaaagc 540
aacataagct gggctaaagg tttaaaattt gaagatggag ccatagcaac caacattgga 600
aatgggttag agtttggaag cagtagtaca gaaacaggtg ttgatgatgc ttacccaatc 660
caagttaaac ttggatctgg ccttagcttt gacagtacag gagccataat ggctggtaac 720
aaagaagacg ataaactcac tttgtggaca acacctgatc catcgccaaa ctgtcaaata 780
ctcgcagaaa atgatgcaaa actaacactt tgcttgacta aatgtggtag tcaaatactg 840
gccactgtgt cagtcttagt tgtaggaagt ggaaacctaa accccattac tggcaccgta 900
agcagtgctc aggtgtttct acgttttgat gcaaacggtg ttcttttaac agaacattct 960
acactaaaaa aatactgggg gtataggcag ggagatagca tagatggcac tccatatacc 1020
aatgctgtag gattcatgcc caatttaaaa gcttatccaa agtcacaaag ttctactact 1080
aaaaataata tagtagggca agtatacatg aatggagatg tttcaaaacc tatgcttctc 1140
actataaccc tcaatggtac tgatgacagc aacagtacat attcaatgtc attttcatac 1200
acctggacta atggaagcta tgttggagca acatttgggg ctaactctta taccttctca 1260
tacatcgccc aagaatga                                                1278
```

<210> 77
<211> 425
<212> PRT
<213> Chimpanzee Adenovirus- ChAd 63 Fiber

<400> 77

```
Met Ser Lys Lys Arg Val Arg Val Asp Asp Asp Phe Asp Pro Val Tyr
 1               5                  10                  15
Pro Tyr Asp Ala Asp Asn Ala Pro Thr Val Pro Phe Ile Asn Pro Pro
            20                  25                  30
Phe Val Ser Ser Asp Gly Phe Gln Glu Lys Pro Leu Gly Val Leu Ser
        35                  40                  45
Leu Arg Leu Ala Asp Pro Val Thr Thr Lys Asn Gly Glu Ile Thr Leu
    50                  55                  60
Lys Leu Gly Glu Gly Val Asp Leu Asp Ser Ser Gly Lys Leu Ile Ser
65                  70                  75                  80
Asn Thr Ala Thr Lys Ala Ala Ala Pro Leu Ser Phe Ser Asn Asn Thr
                85                  90                  95
Ile Ser Leu Asn Met Asp His Pro Phe Tyr Thr Lys Asp Gly Lys Leu
            100                 105                 110
Ser Leu Gln Val Ser Pro Pro Leu Asn Ile Leu Arg Thr Ser Ile Leu
        115                 120                 125
Asn Thr Leu Ala Leu Gly Phe Gly Ser Gly Leu Gly Leu Arg Gly Ser
    130                 135                 140
Ala Leu Ala Val Gln Leu Val Ser Pro Leu Thr Phe Asp Thr Asp Gly
145                 150                 155                 160
Asn Ile Lys Leu Thr Leu Asp Arg Gly Leu His Val Thr Thr Gly Asp
                165                 170                 175
Ala Ile Glu Ser Asn Ile Ser Trp Ala Lys Gly Leu Lys Phe Glu Asp
            180                 185                 190
Gly Ala Ile Ala Thr Asn Ile Gly Asn Gly Leu Glu Phe Gly Ser Ser
        195                 200                 205
Ser Thr Glu Thr Gly Val Asp Asp Ala Tyr Pro Ile Gln Val Lys Leu
    210                 215                 220
Gly Ser Gly Leu Ser Phe Asp Ser Thr Gly Ala Ile Met Ala Gly Asn
225                 230                 235                 240
Lys Glu Asp Asp Lys Leu Thr Leu Trp Thr Thr Pro Asp Pro Ser Pro
                245                 250                 255
Asn Cys Gln Ile Leu Ala Glu Asn Asp Ala Lys Leu Thr Leu Cys Leu
```

```
            260                 265                 270
Thr Lys Cys Gly Ser Gln Ile Leu Ala Thr Val Ser Val Leu Val Val
        275                 280                 285
Gly Ser Gly Asn Leu Asn Pro Ile Thr Gly Thr Val Ser Ser Ala Gln
    290                 295                 300
Val Phe Leu Arg Phe Asp Ala Asn Gly Val Leu Leu Thr Glu His Ser
305                 310                 315                 320
Thr Leu Lys Lys Tyr Trp Gly Tyr Arg Gln Gly Asp Ser Ile Asp Gly
                325                 330                 335
Thr Pro Tyr Thr Asn Ala Val Gly Phe Met Pro Asn Leu Lys Ala Tyr
            340                 345                 350
Pro Lys Ser Gln Ser Ser Thr Thr Lys Asn Asn Ile Val Gly Gln Val
        355                 360                 365
Tyr Met Asn Gly Asp Val Ser Lys Pro Met Leu Leu Thr Ile Thr Leu
    370                 375                 380
Asn Gly Thr Asp Asp Ser Asn Ser Thr Tyr Ser Met Ser Phe Ser Tyr
385                 390                 395                 400
Thr Trp Thr Asn Gly Ser Tyr Val Gly Ala Thr Phe Gly Ala Asn Ser
                405                 410                 415
Tyr Thr Phe Ser Tyr Ile Ala Gln Glu
            420                 425
```

<210> 78
<211> 1338
<212> DNA
<213> Chimpanzee Adenovirus- ChAd 82 Fiber

<400> 78

```
atgtccaaaa agcgcgcgcg ggtggatgat gacttcgacc ccgtgtaccc ctacgatgca 60
gacaacgcac cgactgtgcc cttcatcaac cctcccttcg tctcttcaga tggattccaa 120
gaaaagcccc tgggggtgtt gtccctgcga ctggccgatc ccgtcaccac caagaacggg 180
gctgtcaccc tcaagctggg ggaggggggtg gacctcgacg actcgggaaa actcatctcc 240
aaaaatgcca ccaaggccac tgcccctctc agtatttcca acaacaccat ttcccttaac 300
atggataccc ctctttacaa caacaatgga aagctaggta tgaaggtaac cgcaccatta 360
aagatattag acacagatct actaaaaaca cttgttgttg cttatgggca gggattagga 420
acaaacacca atggtgctct tgttgcccaa ctagcatacc cacttgtttt taataccgct 480
agcaaaattg cccttaattt aggcaatgga ccattaaaag tggatgcaaa tagactgaac 540
attaattgca aaagaggtat ctatgtcact accacaaaag atgcactgga gattaatatc 600
agttgggcaa atgctatgac atttatagga aatgccattg gtgtcaatat tgacacaaaa 660
aaaggcctac agttcggcac ttcaagcact gaaacagatg ttaaaaatgc ttttccactc 720
caagtaaaac ttggagctgg tcttacattt gacagcacag gtgccattgt tgcttggaac 780
aaagaagatg acaaacttac actgtggacc acagccgatc catctccaaa ctgtcacata 840
tattctgcaa aggatgctaa gcttacactc tgcttgacaa agtgtggtag tcagatactg 900
ggcactgttt ctctcatagc tgttgatact ggtagcttaa atccaataac aggaaaagta 960
accactgctc ttgtttcact taaattcgat gccaatggag ttttgcaagc cagttcaaca 1020
ctagataaag aatattggaa tttcagaaaa ggagatgtga cacctgctga cccctacact 1080
aatgctatag gctttatgcc caaccttaat gcatacccaa aaaacacaaa cgcagctgca 1140
aaaagtcaca ttgttggaaa agtataccta catggggatg taagcaagcc actagacttg 1200
ataattacat ttaatgaaac cagtgatgaa tcctgtactt attgcattaa ctttcagtgg 1260
cggtggggaa ctgaccaata taaagatgaa acacttgcag tcagttcatt caccttctca 1320
tacattgcta aagaataa                                              1338
```

<210> 79
<211> 445

<212> PRT
<213> Chimpanzee Adenovirus- ChAd 82 Fiber

<400> 79
Met Ser Lys Lys Arg Ala Arg Val Asp Asp Asp Phe Asp Pro Val Tyr
 1   5   10   15
Pro Tyr Asp Ala Asp Asn Ala Pro Thr Val Pro Phe Ile Asn Pro Pro
            20   25   30
Phe Val Ser Ser Asp Gly Phe Gln Glu Lys Pro Leu Gly Val Leu Ser
        35   40   45
Leu Arg Leu Ala Asp Pro Val Thr Thr Lys Asn Gly Ala Val Thr Leu
    50   55   60
Lys Leu Gly Glu Gly Val Asp Leu Asp Asp Ser Gly Lys Leu Ile Ser
65   70   75   80
Lys Asn Ala Thr Lys Ala Thr Ala Pro Leu Ser Ile Ser Asn Asn Thr
                85   90   95
Ile Ser Leu Asn Met Asp Thr Pro Leu Tyr Asn Asn Asn Gly Lys Leu
            100   105   110
Gly Met Lys Val Thr Ala Pro Leu Lys Ile Leu Asp Thr Asp Leu Leu
        115   120   125
Lys Thr Leu Val Val Ala Tyr Gly Gln Gly Leu Gly Thr Asn Thr Asn
    130   135   140
Gly Ala Leu Val Ala Gln Leu Ala Tyr Pro Leu Val Phe Asn Thr Ala
145   150   155   160
Ser Lys Ile Ala Leu Asn Leu Gly Asn Gly Pro Leu Lys Val Asp Ala
                165   170   175
Asn Arg Leu Asn Ile Asn Cys Lys Arg Gly Ile Tyr Val Thr Thr Thr
            180   185   190
Lys Asp Ala Leu Glu Ile Asn Ile Ser Trp Ala Asn Ala Met Thr Phe
        195   200   205
Ile Gly Asn Ala Ile Gly Val Asn Ile Asp Thr Lys Lys Gly Leu Gln
    210   215   220
Phe Gly Thr Ser Ser Thr Glu Thr Asp Val Lys Asn Ala Phe Pro Leu
225   230   235   240
Gln Val Lys Leu Gly Ala Gly Leu Thr Phe Asp Ser Thr Gly Ala Ile
                245   250   255
Val Ala Trp Asn Lys Glu Asp Asp Lys Leu Thr Leu Trp Thr Thr Ala
            260   265   270
Asp Pro Ser Pro Asn Cys His Ile Tyr Ser Ala Lys Asp Ala Lys Leu
        275   280   285
Thr Leu Cys Leu Thr Lys Cys Gly Ser Gln Ile Leu Gly Thr Val Ser
    290   295   300
Leu Ile Ala Val Asp Thr Gly Ser Leu Asn Pro Ile Thr Gly Lys Val
305   310   315   320
Thr Thr Ala Leu Val Ser Leu Lys Phe Asp Ala Asn Gly Val Leu Gln
                325   330   335
Ala Ser Ser Thr Leu Asp Lys Glu Tyr Trp Asn Phe Arg Lys Gly Asp
            340   345   350
Val Thr Pro Ala Asp Pro Tyr Thr Asn Ala Ile Gly Phe Met Pro Asn
        355   360   365
Leu Asn Ala Tyr Pro Lys Asn Thr Asn Ala Ala Ala Lys Ser His Ile
    370   375   380
Val Gly Lys Val Tyr Leu His Gly Asp Val Ser Lys Pro Leu Asp Leu
385   390   395   400
Ile Ile Thr Phe Asn Glu Thr Ser Asp Glu Ser Cys Thr Tyr Cys Ile

```
                405                 410                 415
Asn Phe Gln Trp Arg Trp Gly Thr Asp Gln Tyr Lys Asp Glu Thr Leu
            420                 425                 430
Ala Val Ser Ser Phe Thr Phe Ser Tyr Ile Ala Lys Glu
        435                 440                 445
```

<210> 80
<211> 445
<212> PRT
<213> Chimpanzee Adenovirus- CV23/Pan5 Fiber

<400> 80

```
Met Ser Lys Lys Arg Val Arg Val Asp Asp Asp Phe Asp Pro Val Tyr
 1               5                  10                  15
Pro Tyr Asp Ala Asp Asn Ala Pro Thr Val Pro Phe Ile Asn Pro Pro
            20                  25                  30
Phe Val Ser Ser Asp Gly Phe Gln Glu Lys Pro Leu Gly Val Leu Ser
        35                  40                  45
Leu Arg Leu Ala Asp Pro Val Thr Thr Lys Asn Gly Glu Ile Thr Leu
    50                  55                  60
Lys Leu Gly Asp Gly Val Asp Leu Asp Ser Ser Gly Lys Leu Ile Ser
65                  70                  75                  80
Asn Thr Ala Thr Lys Ala Ala Ala Pro Leu Ser Phe Ser Asn Asn Thr
                85                  90                  95
Ile Ser Leu Asn Met Asp Thr Pro Phe Tyr Asn Asn Asn Gly Lys Leu
            100                 105                 110
Gly Met Lys Val Thr Ala Pro Leu Lys Ile Leu Asp Thr Asp Leu Leu
        115                 120                 125
Lys Thr Leu Val Val Ala Tyr Gly Gln Gly Leu Gly Thr Asn Thr Thr
    130                 135                 140
Gly Ala Leu Val Ala Gln Leu Ala Ser Pro Leu Ala Phe Asp Ser Asn
145                 150                 155                 160
Ser Lys Ile Ala Leu Asn Leu Gly Asn Gly Pro Leu Lys Val Asp Ala
                165                 170                 175
Asn Arg Leu Asn Ile Asn Cys Asn Arg Gly Leu Tyr Val Thr Thr Thr
            180                 185                 190
Lys Asp Ala Leu Glu Ala Asn Ile Ser Trp Ala Asn Ala Met Thr Phe
        195                 200                 205
Ile Gly Asn Ala Met Gly Val Asn Ile Asp Thr Gln Lys Gly Leu Gln
    210                 215                 220
Phe Gly Thr Thr Ser Thr Val Ala Asp Val Lys Asn Ala Tyr Pro Ile
225                 230                 235                 240
Gln Ile Lys Leu Gly Ala Gly Leu Thr Phe Asp Ser Thr Gly Ala Ile
                245                 250                 255
Val Ala Trp Asn Lys Asp Asp Asp Lys Leu Thr Leu Trp Thr Thr Ala
            260                 265                 270
Asp Pro Ser Pro Asn Cys His Ile Tyr Ser Glu Lys Asp Ala Lys Leu
        275                 280                 285
Thr Leu Cys Leu Thr Lys Cys Gly Ser Gln Ile Leu Gly Thr Val Ser
    290                 295                 300
Leu Ile Ala Val Asp Thr Gly Ser Leu Asn Pro Ile Thr Gly Thr Val
305                 310                 315                 320
Thr Thr Ala Leu Val Ser Leu Lys Phe Asp Ala Asn Gly Val Leu Gln
                325                 330                 335
```

```
Ser Ser Ser Thr Leu Asp Ser Asp Tyr Trp Asn Phe Arg Gln Gly Asp
            340                 345                 350
Val Thr Pro Ala Glu Ala Tyr Thr Asn Ala Ile Gly Phe Met Pro Asn
        355                 360                 365
Leu Lys Ala Tyr Pro Lys Asn Thr Ser Gly Ala Ala Lys Ser His Ile
    370                 375                 380
Val Gly Lys Val Tyr Leu His Gly Asp Thr Gly Lys Pro Leu Asp Leu
385                 390                 395                 400
Ile Ile Thr Phe Asn Glu Thr Ser Asp Glu Ser Cys Thr Tyr Cys Ile
                405                 410                 415
Asn Phe Gln Trp Gln Trp Gly Ala Asp Gln Tyr Lys Asn Glu Thr Leu
            420                 425                 430
Ala Val Ser Ser Phe Thr Phe Ser Tyr Ile Ala Lys Glu
        435                 440                 445
```

<210> 81
<211> 443
<212> PRT
<213> Chimpanzee Adenovirus- CV32/Pan6 Fiber

<400> 81

```
Met Ser Lys Lys Arg Val Arg Val Asp Asp Asp Phe Asp Pro Val Tyr
 1               5                  10                  15
Pro Tyr Asp Ala Asp Asn Ala Pro Thr Val Pro Phe Ile Asn Pro Pro
            20                  25                  30
Phe Val Ser Ser Asp Gly Phe Gln Glu Lys Pro Leu Gly Val Leu Ser
        35                  40                  45
Leu Arg Leu Ala Asp Pro Val Thr Thr Lys Asn Gly Glu Ile Thr Leu
    50                  55                  60
Lys Leu Gly Glu Gly Val Asp Leu Asp Ser Ser Gly Lys Leu Ile Ser
65                  70                  75                  80
Asn Thr Ala Thr Lys Ala Ala Ala Pro Leu Ser Ile Ser Asn Asn Thr
                85                  90                  95
Ile Ser Leu Lys Thr Ala Ala Pro Phe Tyr Asn Asn Asn Gly Thr Leu
            100                 105                 110
Ser Leu Asn Val Ser Thr Pro Leu Ala Val Phe Pro Thr Phe Asn Thr
        115                 120                 125
Leu Gly Ile Ser Leu Gly Asn Gly Leu Gln Thr Ser Asn Lys Leu Leu
    130                 135                 140
Thr Val Gln Leu Thr His Pro Leu Thr Phe Ser Ser Asn Ser Ile Thr
145                 150                 155                 160
Val Lys Thr Asp Lys Gly Leu Tyr Ile Asn Ser Ser Gly Asn Arg Gly
                165                 170                 175
Leu Glu Ala Asn Ile Ser Leu Lys Arg Gly Leu Val Phe Asp Gly Asn
            180                 185                 190
Ala Ile Ala Thr Tyr Ile Gly Asn Gly Leu Asp Tyr Gly Ser Tyr Asp
        195                 200                 205
Ser Asp Gly Lys Thr Arg Pro Val Ile Thr Lys Ile Gly Ala Gly Leu
    210                 215                 220
Asn Phe Asp Ala Asn Lys Ala Ile Ala Val Lys Leu Gly Thr Gly Leu
225                 230                 235                 240
Ser Phe Asp Ser Ala Gly Ala Leu Thr Ala Gly Asn Lys Gln Asp Asp
                245                 250                 255
Lys Leu Thr Leu Trp Thr Thr Pro Asp Pro Ser Pro Asn Cys Gln Leu
```

```
            260                 265                 270
Leu Ser Asp Arg Asp Ala Lys Phe Thr Leu Cys Leu Thr Lys Cys Gly
        275                 280                 285
Ser Gln Ile Leu Gly Thr Val Ala Val Ala Ala Val Thr Val Gly Ser
    290                 295                 300
Ala Leu Asn Pro Ile Asn Asp Thr Val Lys Ser Ala Ile Val Phe Leu
305                 310                 315                 320
Arg Phe Asp Ser Asp Gly Val Leu Met Ser Asn Ser Ser Met Val Gly
                325                 330                 335
Asp Tyr Trp Asn Phe Arg Glu Gly Gln Thr Thr Gln Ser Val Ala Tyr
            340                 345                 350
Thr Asn Ala Val Gly Phe Met Pro Asn Ile Gly Ala Tyr Pro Lys Thr
        355                 360                 365
Gln Ser Lys Thr Pro Lys Asn Ser Ile Val Ser Gln Val Tyr Leu Thr
    370                 375                 380
Gly Glu Thr Thr Met Pro Met Thr Leu Thr Ile Thr Phe Asn Gly Thr
385                 390                 395                 400
Asp Glu Lys Asp Thr Thr Pro Val Ser Thr Tyr Ser Met Thr Phe Thr
                405                 410                 415
Trp Gln Trp Thr Gly Asp Tyr Lys Asp Lys Asn Ile Thr Phe Ala Thr
            420                 425                 430
Asn Ser Phe Ser Phe Ser Tyr Ile Ala Gln Glu
        435                 440
```

<210> 82
<211> 443
<212> PRT
<213> Chimpanzee Adenovirus- CV33/Pan7 Fiber

<400> 82

```
Met Ser Lys Lys Arg Val Arg Val Asp Asp Asp Phe Asp Pro Val Tyr
 1               5                  10                  15
Pro Tyr Asp Ala Asp Asn Ala Pro Thr Val Pro Phe Ile Asn Pro Pro
            20                  25                  30
Phe Val Ser Ser Asp Gly Phe Gln Glu Lys Pro Leu Gly Val Leu Ser
        35                  40                  45
Leu Arg Leu Ala Asp Pro Val Thr Thr Lys Asn Gly Glu Ile Thr Leu
    50                  55                  60
Lys Leu Gly Glu Gly Val Asp Leu Asp Ser Ser Gly Lys Leu Ile Ser
65                  70                  75                  80
Asn Thr Ala Thr Lys Ala Ala Ala Pro Leu Ser Phe Ser Asn Asn Thr
                85                  90                  95
Ile Ser Leu Asn Met Asp Thr Pro Leu Tyr Thr Lys Asp Gly Lys Leu
            100                 105                 110
Ser Leu Gln Val Ser Pro Pro Leu Asn Ile Leu Lys Ser Thr Ile Leu
        115                 120                 125
Asn Thr Leu Ala Val Ala Tyr Gly Ser Gly Leu Gly Leu Ser Gly Gly
    130                 135                 140
Thr Ala Leu Ala Val Gln Leu Ala Ser Pro Leu Thr Phe Asp Glu Lys
145                 150                 155                 160
Gly Asn Ile Lys Ile Asn Leu Ala Ser Gly Pro Leu Thr Val Asp Ala
                165                 170                 175
Ser Arg Leu Ser Ile Asn Cys Lys Arg Gly Val Thr Val Thr Thr Ser
            180                 185                 190
```

```
Gly Asp Ala Ile Glu Ser Asn Ile Ser Trp Pro Lys Gly Ile Arg Phe
        195                 200                 205
Glu Gly Asn Gly Ile Ala Ala Asn Ile Gly Arg Gly Leu Glu Phe Gly
    210                 215                 220
Thr Thr Ser Thr Glu Thr Asp Val Thr Asp Ala Tyr Pro Ile Gln Val
225                 230                 235                 240
Lys Leu Gly Thr Gly Leu Thr Phe Asp Ser Thr Gly Ala Ile Val Ala
                245                 250                 255
Trp Asn Lys Glu Asp Asp Lys Leu Thr Leu Trp Thr Thr Ala Asp Pro
            260                 265                 270
Ser Pro Asn Cys Lys Ile Tyr Ser Glu Lys Asp Ala Lys Leu Thr Leu
        275                 280                 285
Cys Leu Thr Lys Cys Gly Ser Gln Ile Leu Gly Thr Val Thr Val Leu
    290                 295                 300
Ala Val Asn Asn Gly Ser Leu Asn Pro Ile Thr Asn Thr Val Ser Thr
305                 310                 315                 320
Ala Leu Val Ser Leu Lys Phe Asp Ala Ser Gly Val Leu Leu Ser Ser
                325                 330                 335
Ser Thr Leu Asp Lys Glu Tyr Trp Asn Phe Arg Lys Gly Asp Val Thr
            340                 345                 350
Pro Ala Glu Pro Tyr Thr Asn Ala Ile Gly Phe Met Pro Asn Ile Lys
        355                 360                 365
Ala Tyr Pro Lys Asn Thr Ser Ala Ala Ser Lys Ser His Ile Val Ser
    370                 375                 380
Gln Val Tyr Leu Asn Gly Asp Glu Ala Lys Pro Leu Met Leu Ile Ile
385                 390                 395                 400
Thr Phe Asn Glu Thr Glu Asp Ala Thr Cys Thr Tyr Ser Ile Thr Phe
                405                 410                 415
Gln Trp Lys Trp Asp Ser Thr Lys Tyr Thr Gly Glu Thr Leu Ala Thr
            420                 425                 430
Ser Ser Phe Thr Phe Ser Tyr Ile Ala Gln Glu
        435                 440
```

<210> 83
<211> 543
<212> PRT
<213> Chimpanzee Adenovirus- ChAd 3 Fiber

<400> 83

```
Met Lys Arg Thr Lys Thr Ser Asp Glu Ser Phe Asn Pro Val Tyr Pro
 1               5                  10                  15
Tyr Asp Thr Glu Ser Gly Pro Pro Ser Val Pro Phe Leu Thr Pro Pro
            20                  25                  30
Phe Val Ser Pro Asp Gly Phe Gln Glu Ser Pro Pro Gly Val Leu Ser
        35                  40                  45
Leu Asn Leu Ala Glu Pro Leu Val Thr Ser His Gly Met Leu Ala Leu
    50                  55                  60
Lys Met Gly Ser Gly Leu Ser Leu Asp Asp Ala Gly Asn Leu Thr Ser
65                  70                  75                  80
Gln Asp Ile Thr Thr Ala Ser Pro Pro Leu Lys Lys Thr Lys Thr Asn
                85                  90                  95
Leu Ser Leu Glu Thr Ser Ser Pro Leu Thr Val Ser Thr Ser Gly Ala
            100                 105                 110
Leu Thr Val Ala Ala Ala Ala Pro Leu Ala Val Ala Gly Thr Ser Leu
```

```
        115                 120                 125
Thr Met Gln Ser Glu Ala Pro Leu Thr Val Gln Asp Ala Lys Leu Thr
    130                 135                 140
Leu Ala Thr Lys Gly Pro Leu Thr Val Ser Glu Gly Lys Leu Ala Leu
145                 150                 155                 160
Gln Thr Ser Ala Pro Leu Thr Ala Ala Asp Ser Ser Thr Leu Thr Val
                165                 170                 175
Ser Ala Thr Pro Pro Ile Asn Val Ser Ser Gly Ser Leu Gly Leu Asp
            180                 185                 190
Met Glu Asp Pro Met Tyr Thr His Asp Gly Lys Leu Gly Ile Arg Ile
        195                 200                 205
Gly Gly Pro Leu Arg Val Val Asp Ser Leu His Thr Leu Thr Val Val
    210                 215                 220
Thr Gly Asn Gly Leu Thr Val Asp Asn Asn Ala Leu Gln Thr Arg Val
225                 230                 235                 240
Thr Gly Ala Leu Gly Tyr Asp Thr Ser Gly Asn Leu Gln Leu Arg Ala
                245                 250                 255
Ala Gly Gly Met Arg Ile Asp Ala Asn Gly Gln Leu Ile Leu Asn Val
            260                 265                 270
Ala Tyr Pro Phe Asp Ala Gln Asn Asn Leu Ser Leu Arg Leu Gly Gln
        275                 280                 285
Gly Pro Leu Tyr Ile Asn Thr Asp His Asn Leu Asp Leu Asn Cys Asn
    290                 295                 300
Arg Gly Leu Thr Thr Thr Thr Thr Asn Asn Thr Lys Lys Leu Glu Thr
305                 310                 315                 320
Lys Ile Ser Ser Gly Leu Asp Tyr Asp Thr Asn Gly Ala Val Ile Ile
                325                 330                 335
Lys Leu Gly Thr Gly Leu Ser Phe Asp Asn Thr Gly Ala Leu Thr Val
            340                 345                 350
Gly Asn Thr Gly Asp Asp Lys Leu Thr Leu Trp Thr Thr Pro Asp Pro
        355                 360                 365
Ser Pro Asn Cys Arg Ile His Ser Asp Lys Asp Cys Lys Phe Thr Leu
    370                 375                 380
Val Leu Thr Lys Cys Gly Ser Gln Ile Leu Ala Ser Val Ala Ala Leu
385                 390                 395                 400
Ala Val Ser Gly Asn Leu Ala Ser Ile Thr Gly Thr Val Ala Ser Val
                405                 410                 415
Thr Ile Phe Leu Arg Phe Asp Gln Asn Gly Val Leu Met Glu Asn Ser
            420                 425                 430
Ser Leu Asp Arg Gln Tyr Trp Asn Phe Arg Asn Gly Asn Ser Thr Asn
        435                 440                 445
Ala Ala Pro Tyr Thr Asn Ala Val Gly Phe Met Pro Asn Leu Ala Ala
    450                 455                 460
Tyr Pro Lys Thr Gln Ser Gln Thr Ala Lys Asn Asn Ile Val Ser Gln
465                 470                 475                 480
Val Tyr Leu Asn Gly Asp Lys Ser Lys Pro Met Thr Leu Thr Ile Thr
                485                 490                 495
Leu Asn Gly Thr Asn Glu Ser Ser Glu Thr Ser Gln Val Ser His Tyr
            500                 505                 510
Ser Met Ser Phe Thr Trp Ala Trp Glu Ser Gly Gln Tyr Ala Thr Glu
        515                 520                 525
Thr Phe Ala Thr Asn Ser Phe Thr Phe Ser Tyr Ile Ala Glu Gln
    530                 535                 540
```

<210> 84
<211> 445
<212> PRT
<213> Chimpanzee Adenovirus- ChAd 6 Fiber

<400> 84
Met Ser Lys Lys Arg Ala Arg Val Asp Asp Asp Phe Asp Pro Val Tyr
 1   5   10   15
Pro Tyr Asp Ala Asp Asn Ala Pro Thr Val Pro Phe Ile Asn Pro Pro
            20   25   30
Phe Val Ser Ser Asp Gly Phe Gln Glu Lys Pro Leu Gly Val Leu Ser
        35   40   45
Leu Arg Leu Ala Asp Pro Val Thr Thr Lys Asn Gly Ala Val Thr Leu
    50   55   60
Lys Leu Gly Glu Gly Val Asp Leu Asp Asp Ser Gly Lys Leu Ile Ser
65   70   75   80
Lys Asn Ala Thr Lys Ala Thr Ala Pro Leu Ser Ile Ser Asn Asn Thr
                85   90   95
Ile Ser Leu Asn Met Asp Thr Pro Leu Tyr Asn Asn Asn Gly Lys Leu
            100   105   110
Gly Met Lys Val Thr Ala Pro Leu Lys Ile Leu Asp Thr Asp Leu Leu
        115   120   125
Lys Thr Leu Val Val Ala Tyr Gly Gln Gly Leu Gly Thr Asn Thr Asn
    130   135   140
Gly Ala Leu Val Ala Gln Leu Ala Tyr Pro Leu Val Phe Asn Thr Ala
145   150   155   160
Ser Lys Ile Ala Leu Asn Leu Gly Asn Gly Pro Leu Lys Val Asp Ala
                165   170   175
Asn Arg Leu Asn Ile Asn Cys Lys Arg Gly Ile Tyr Val Thr Thr Thr
            180   185   190
Lys Asp Ala Leu Glu Ile Asn Ile Ser Trp Ala Asn Ala Met Thr Phe
        195   200   205
Ile Gly Asn Ala Ile Gly Val Asn Ile Asp Thr Lys Lys Gly Leu Gln
    210   215   220
Phe Gly Thr Ser Ser Thr Glu Thr Asp Val Lys Asn Ala Phe Pro Leu
225   230   235   240
Gln Val Lys Leu Gly Ala Gly Leu Thr Phe Asp Ser Thr Gly Ala Ile
                245   250   255
Val Ala Trp Asn Lys Glu Asp Asp Lys Leu Thr Leu Trp Thr Thr Ala
            260   265   270
Asp Pro Ser Pro Asn Cys His Ile Tyr Ser Ala Lys Asp Ala Lys Leu
        275   280   285
Thr Leu Cys Leu Thr Lys Cys Gly Ser Gln Ile Leu Gly Thr Val Ser
    290   295   300
Leu Ile Ala Val Asp Thr Gly Ser Leu Asn Pro Ile Thr Gly Lys Val
305   310   315   320
Thr Thr Ala Leu Val Ser Leu Lys Phe Asp Ala Asn Gly Val Leu Gln
                325   330   335
Ala Ser Ser Thr Leu Asp Lys Glu Tyr Trp Asn Phe Arg Lys Gly Asp
            340   345   350
Val Thr Pro Ala Asp Pro Tyr Thr Asn Ala Ile Gly Phe Met Pro Asn
        355   360   365
Leu Asn Ala Tyr Pro Lys Asn Thr Asn Ala Ala Ala Lys Ser His Ile
    370   375   380
Val Gly Lys Val Tyr Leu His Gly Asp Glu Ser Lys Pro Leu Asp Leu

```
385                 390                 395                 400
Ile Ile Thr Phe Asn Glu Thr Ser Asp Glu Ser Cys Thr Tyr Cys Ile
                405                 410                 415
Asn Phe Gln Trp Gln Trp Gly Thr Asp Gln Tyr Lys Asp Glu Thr Leu
            420                 425                 430
Ala Val Ser Ser Phe Thr Phe Ser Tyr Ile Ala Lys Glu
        435                 440                 445
```

<210> 85
<211> 322
<212> PRT
<213> Chimpanzee Adenovirus- C1 Fiber

<400> 85

```
Met Ala Lys Arg Thr Arg Leu Ser Ser Ser Phe Asn Pro Val Tyr Pro
 1               5                  10                  15
Tyr Glu Asp Glu Asn Ser Ser His Pro Phe Ile Asn Pro Gly Phe Ile
            20                  25                  30
Ser Pro Asn Gly Phe Thr Gln Ser Pro Asp Gly Val Leu Thr Leu Asn
        35                  40                  45
Cys Val Ala Pro Leu Thr Thr Ala Asn Gly Ala Leu Asp Ile Lys Val
    50                  55                  60
Gly Gly Gly Leu Lys Val Asn Ser Thr Asp Gly Phe Leu Glu Glu Asn
65                  70                  75                  80
Ile Asn Ile Thr Ser Pro Leu Thr Lys Ser Asn His Ser Ile Gly Leu
                85                  90                  95
Glu Trp Ser Asp Gly Leu Gln Thr Asn Glu Ala Lys Leu Cys Val Lys
            100                 105                 110
Leu Gly Lys Gly Leu Val Phe Asp Ser Ser Ser Ala Ile Ala Met Glu
        115                 120                 125
Asn Asn Thr Leu Trp Thr Gly Ala Lys Pro Ser Ala Asn Cys Val Ile
    130                 135                 140
Lys Glu Gly Glu Asp Ser Pro Asp Cys Lys Leu Thr Leu Val Leu Val
145                 150                 155                 160
Lys Asn Gly Gly Leu Val Asn Gly Tyr Ile Thr Leu Met Gly Asp Ser
                165                 170                 175
Glu Tyr Thr Asn Thr Leu Phe Lys Asn Lys Gln Val Thr Ile Asp Val
            180                 185                 190
Asn Leu Ala Phe Asp Asn Thr Gly Gln Ile Ile Thr Tyr Leu Ser Ser
        195                 200                 205
Leu Lys Ser Asn Leu Asn Phe Lys Asp Asn Gln Asn Met Ala Thr Gly
    210                 215                 220
Thr Ile Thr Ser Ala Lys Gly Phe Met Pro Ser Thr Thr Ala Tyr Pro
225                 230                 235                 240
Phe Ile Thr Tyr Ala Thr Gln Ser Leu Asn Glu Asp Tyr Ile Tyr Gly
                245                 250                 255
Glu Cys Tyr Tyr Lys Ser Thr Asn Gly Thr Leu Phe Pro Leu Lys Val
            260                 265                 270
Thr Val Thr Leu Asn Arg Arg Met Ser Ala Ser Gly Met Ala Tyr Ala
        275                 280                 285
Met Asn Phe Ser Trp Ser Leu Asn Ala Glu Glu Ala Pro Glu Thr Thr
    290                 295                 300
Glu Val Thr Leu Ile Thr Ser Pro Phe Phe Phe Ser Tyr Ile Arg Glu
305                 310                 315                 320
```

Asp Asp

<210> 86
<211> 425
<212> PRT
<213> Chimpanzee Adenovirus- CV68 Fiber

<400> 86
Met Ser Lys Lys Arg Val Arg Val Asp Asp Asp Phe Asp Pro Val Tyr
 1   5   10   15
Pro Tyr Asp Ala Asp Asn Ala Pro Thr Val Pro Phe Ile Asn Pro Pro
            20   25   30
Phe Val Ser Ser Asp Gly Phe Gln Glu Lys Pro Leu Gly Val Leu Ser
        35   40   45
Leu Arg Leu Ala Asp Pro Val Thr Thr Lys Asn Gly Glu Ile Thr Leu
    50   55   60
Lys Leu Gly Glu Gly Val Asp Leu Asp Ser Ser Gly Lys Leu Ile Ser
65   70   75   80
Asn Thr Ala Thr Lys Ala Ala Ala Pro Leu Ser Phe Ser Asn Asn Thr
                85   90   95
Ile Ser Leu Asn Met Asp His Pro Phe Tyr Thr Lys Asp Gly Lys Leu
            100   105   110
Ser Leu Gln Val Ser Pro Pro Leu Asn Ile Leu Arg Thr Ser Ile Leu
        115   120   125
Asn Thr Leu Ala Leu Gly Phe Gly Ser Gly Leu Gly Leu Arg Gly Ser
    130   135   140
Ala Leu Ala Val Gln Leu Val Ser Pro Leu Thr Phe Asp Thr Asp Gly
145   150   155   160
Asn Ile Lys Leu Thr Leu Asp Arg Gly Leu His Val Thr Thr Gly Asp
                165   170   175
Ala Ile Glu Ser Asn Ile Ser Trp Ala Lys Gly Leu Lys Phe Glu Asp
            180   185   190
Gly Ala Ile Ala Thr Asn Ile Gly Asn Gly Leu Glu Phe Gly Ser Ser
        195   200   205
Ser Thr Glu Thr Gly Val Asp Asp Ala Tyr Pro Ile Gln Val Lys Leu
    210   215   220
Gly Ser Gly Leu Ser Phe Asp Ser Thr Gly Ala Ile Met Ala Gly Asn
225   230   235   240
Lys Glu Asp Asp Lys Leu Thr Leu Trp Thr Thr Pro Asp Pro Ser Pro
                245   250   255
Asn Cys Gln Ile Leu Ala Glu Asn Asp Ala Lys Leu Thr Leu Cys Leu
            260   265   270
Thr Lys Cys Gly Ser Gln Ile Leu Ala Thr Val Ser Val Leu Val Val
        275   280   285
Gly Ser Gly Asn Leu Asn Pro Ile Thr Gly Thr Val Ser Ser Ala Gln
    290   295   300
Val Phe Leu Arg Phe Asp Ala Asn Gly Val Leu Leu Thr Glu His Ser
305   310   315   320
Thr Leu Lys Lys Tyr Trp Gly Tyr Arg Gln Gly Asp Ser Ile Asp Gly
                325   330   335
Thr Pro Tyr Thr Asn Ala Val Gly Phe Met Pro Asn Leu Lys Ala Tyr
            340   345   350
Pro Lys Ser Gln Ser Ser Thr Thr Lys Asn Asn Ile Val Gly Gln Val

```
        355                 360                 365
Tyr Met Asn Gly Asp Val Ser Lys Pro Met Leu Leu Thr Ile Thr Leu
    370                 375                 380
Asn Gly Thr Asp Asp Ser Asn Ser Thr Tyr Ser Met Ser Phe Ser Tyr
385                 390                 395                 400
Thr Trp Thr Asn Gly Ser Tyr Val Gly Ala Thr Phe Gly Ala Asn Ser
                405                 410                 415
Tyr Thr Phe Ser Tyr Ile Ala Gln Glu
            420                 425
```

<210> 87
<211> 954
<212> PRT
<213> Chimpanzee Adenovirus- ChAd20 Hexon

<400> 87

```
Met Ala Thr Pro Ser Met Met Pro Gln Trp Ser Tyr Met His Ile Ser
 1               5                  10                  15
Gly Gln Asp Ala Ser Glu Tyr Leu Ser Pro Gly Leu Val Gln Phe Ala
            20                  25                  30
Arg Ala Thr Glu Ser Tyr Phe Ser Leu Ser Asn Lys Phe Arg Asn Pro
        35                  40                  45
Thr Val Ala Pro Thr His Asp Val Thr Thr Asp Arg Ser Gln Arg Leu
    50                  55                  60
Thr Leu Arg Phe Ile Pro Val Asp Arg Glu Asp Thr Ala Tyr Ser Tyr
65                  70                  75                  80
Lys Ala Arg Phe Thr Leu Ala Val Gly Asp Asn Arg Val Leu Asp Met
                85                  90                  95
Ala Ser Thr Tyr Phe Asp Ile Arg Gly Val Leu Asp Arg Gly Pro Thr
            100                 105                 110
Phe Lys Pro Tyr Ser Gly Thr Ala Tyr Asn Ser Leu Ala Pro Lys Gly
        115                 120                 125
Ala Pro Asn Pro Cys Glu Trp Asp Glu Ala Ala Thr Ala Leu Asp Ile
    130                 135                 140
Asp Leu Asn Ala Glu Asp Asp Glu Glu Ser Asp Glu Ala Gln Gly Glu
145                 150                 155                 160
Ala Asp Gln Gln Lys Thr His Val Phe Gly Gln Ala Pro Tyr Ser Gly
                165                 170                 175
Gln Asn Ile Thr Lys Glu Gly Ile Gln Ile Gly Ile Asp Ala Ala Ser
            180                 185                 190
Gln Ala Gln Thr Pro Val Tyr Ala Asp Lys Thr Phe Gln Pro Glu Pro
        195                 200                 205
Gln Val Gly Glu Ser Gln Trp Asn Glu Thr Glu Ile Ser Tyr Gly Ala
    210                 215                 220
Gly Arg Val Leu Lys Lys Thr Thr Leu Met Lys Pro Cys Tyr Gly Ser
225                 230                 235                 240
Tyr Ala Arg Pro Thr Asn Glu Asn Gly Gly Gln Gly Ile Leu Leu Glu
                245                 250                 255
Gln Asp Gly Lys Lys Glu Ser Gln Val Glu Met Gln Phe Phe Ser Thr
            260                 265                 270
Thr Gln Ala Ala Ala Gly Asn Ser Asp Asn Pro Thr Pro Lys Val Val
        275                 280                 285
Leu Tyr Ser Glu Asp Val Asn Leu Glu Thr Pro Asp Thr His Ile Ser
    290                 295                 300
```

```
Tyr Met Pro Thr Asn Asn Glu Thr Asn Ser Arg Glu Leu Leu Gly Gln
305                 310                 315                 320
Gln Ala Met Pro Asn Arg Pro Asn Tyr Ile Gly Phe Arg Asp Asn Phe
                325                 330                 335
Ile Gly Leu Met Tyr Tyr Asn Ser Thr Gly Asn Met Gly Val Leu Ala
            340                 345                 350
Gly Gln Ala Ser Gln Leu Asn Ala Val Val Asp Leu Gln Asp Arg Asn
        355                 360                 365
Thr Glu Leu Ser Tyr Gln Leu Leu Leu Asp Ser Met Gly Asp Arg Thr
    370                 375                 380
Arg Tyr Phe Ser Met Trp Asn Gln Ala Val Asp Ser Tyr Asp Pro Asp
385                 390                 395                 400
Val Arg Ile Ile Glu Asn His Gly Thr Glu Asp Glu Leu Pro Asn Tyr
                405                 410                 415
Cys Phe Pro Leu Gly Gly Val Ile Asn Thr Glu Thr Phe Thr Lys Val
            420                 425                 430
Lys Pro Lys Ala Ala Gln Asp Ala Gln Trp Glu Lys Asp Ser Glu Phe
        435                 440                 445
Ser Asp Lys Asn Glu Ile Arg Val Gly Asn Asn Phe Ala Met Glu Ile
    450                 455                 460
Asn Leu Asn Ala Asn Leu Trp Arg Asn Phe Leu Tyr Ser Asn Val Ala
465                 470                 475                 480
Leu Tyr Leu Pro Asp Lys Leu Lys Tyr Thr Pro Ser Asn Val Gln Ile
                485                 490                 495
Ser Asn Asn Pro Asn Ser Tyr Asp Tyr Met Asn Lys Arg Val Val Ala
            500                 505                 510
Pro Gly Leu Val Asp Cys Tyr Ile Asn Leu Gly Ala Arg Trp Ser Leu
        515                 520                 525
Asp Tyr Met Asp Asn Val Asn Pro Phe Asn His His Arg Asn Ala Gly
    530                 535                 540
Leu Arg Tyr Arg Ser Met Leu Leu Gly Asn Gly Arg Tyr Val Pro Phe
545                 550                 555                 560
His Ile Gln Val Pro Gln Lys Phe Phe Ala Ile Lys Asn Leu Leu Leu
                565                 570                 575
Leu Pro Gly Ser Tyr Thr Tyr Glu Trp Asn Phe Arg Lys Asp Val Asn
            580                 585                 590
Met Val Leu Gln Ser Ser Leu Gly Asn Asp Leu Arg Val Asp Gly Ala
        595                 600                 605
Ser Ile Lys Phe Glu Ser Ile Cys Leu Tyr Ala Thr Phe Phe Pro Met
    610                 615                 620
Ala His Asn Thr Ala Ser Thr Leu Glu Ala Met Leu Arg Asn Asp Thr
625                 630                 635                 640
Asn Asp Gln Ser Phe Asn Asp Tyr Leu Ser Ala Ala Asn Met Leu Tyr
                645                 650                 655
Pro Ile Pro Ala Asn Ala Thr Asn Val Pro Ile Ser Ile Pro Ser Arg
            660                 665                 670
Asn Trp Ala Ala Phe Arg Gly Trp Ala Phe Thr Arg Leu Lys Thr Lys
        675                 680                 685
Glu Thr Pro Ser Leu Gly Ser Gly Phe Asp Pro Tyr Tyr Thr Tyr Ser
    690                 695                 700
Gly Ser Ile Pro Tyr Leu Asp Gly Thr Phe Tyr Leu Asn His Thr Phe
705                 710                 715                 720
Lys Lys Val Ser Val Thr Phe Asp Ser Ser Val Ser Trp Pro Gly Asn
                725                 730                 735
Asp Arg Leu Leu Thr Pro Asn Glu Phe Glu Ile Lys Arg Ser Val Asp
```

```
            740                 745                 750
Gly Glu Gly Tyr Asn Val Ala Gln Cys Asn Met Thr Lys Asp Trp Phe
        755                 760                 765
Leu Val Gln Met Leu Ala Asn Tyr Asn Ile Gly Tyr Gln Gly Phe Tyr
    770                 775                 780
Ile Pro Glu Ser Tyr Lys Asp Arg Met Tyr Ser Phe Phe Arg Asn Phe
785                 790                 795                 800
Gln Pro Met Ser Arg Gln Val Val Asp Gln Thr Lys Tyr Lys Asp Tyr
                805                 810                 815
Gln Glu Val Gly Ile Ile His Gln His Asn Asn Ser Gly Phe Val Gly
            820                 825                 830
Tyr Leu Ala Pro Thr Met Arg Glu Gly Gln Ala Tyr Pro Ala Asn Phe
        835                 840                 845
Pro Tyr Pro Leu Ile Gly Lys Thr Ala Val Asp Ser Ile Thr Gln Lys
    850                 855                 860
Lys Phe Leu Cys Asp Arg Thr Leu Trp Arg Ile Pro Phe Ser Ser Asn
865                 870                 875                 880
Phe Met Ser Met Gly Ala Leu Ser Asp Leu Gly Gln Asn Leu Leu Tyr
                885                 890                 895
Ala Asn Ser Ala His Ala Leu Asp Met Thr Phe Glu Val Asp Pro Met
            900                 905                 910
Asp Glu Pro Thr Leu Leu Tyr Val Leu Phe Glu Val Phe Asp Val Val
        915                 920                 925
Arg Val His Gln Pro His Arg Gly Val Ile Glu Thr Val Tyr Leu Arg
    930                 935                 940
Thr Pro Phe Ser Ala Gly Asn Ala Thr Thr
945                 950
```

<210> 88
<211> 940
<212> PRT
<213> Chimpanzee Adenovirus- ChAd 4 Hexon

<400> 88

```
Met Ala Thr Pro Ser Met Leu Pro Gln Trp Ala Tyr Met His Ile Ala
 1               5                  10                  15
Gly Gln Asp Ala Ser Glu Tyr Leu Ser Pro Gly Leu Val Gln Phe Ala
            20                  25                  30
Arg Ala Thr Asp Thr Tyr Phe Ser Leu Gly Asn Lys Phe Arg Asn Pro
        35                  40                  45
Thr Val Ala Pro Thr His Asp Val Thr Thr Asp Arg Ser Gln Arg Leu
    50                  55                  60
Thr Leu Arg Phe Val Pro Val Asp Arg Glu Asp Asn Thr Tyr Ser Tyr
65                  70                  75                  80
Lys Val Arg Tyr Thr Leu Ala Val Gly Asp Asn Arg Val Leu Asp Met
                85                  90                  95
Ala Ser Thr Tyr Phe Asp Ile Arg Gly Val Leu Asp Arg Gly Pro Ser
            100                 105                 110
Phe Lys Pro Tyr Ser Gly Thr Ala Tyr Asn Ser Leu Ala Pro Lys Gly
        115                 120                 125
Ala Pro Asn Ser Ser Gln Trp Glu Gln Lys Lys Thr Gly Asn Asn Ala
    130                 135                 140
Asn Gly Asp Thr Glu Asn Val Thr Tyr Gly Val Ala Ala Met Gly Gly
145                 150                 155                 160
```

```
Ile Asp Ile Asp Lys Asn Gly Leu Gln Ile Gly Thr Asp Asp Thr Lys
                  165                 170                 175
Asp Asp Asp Asn Glu Ile Tyr Ala Asp Lys Thr Tyr Gln Pro Glu Pro
             180                 185                 190
Gln Ile Gly Glu Glu Asn Trp Gln Glu Thr Tyr Ser Tyr Tyr Gly Gly
         195                 200                 205
Arg Ala Leu Lys Lys Asp Thr Lys Met Lys Pro Cys Tyr Gly Ser Phe
     210                 215                 220
Ala Arg Pro Thr Asn Val Lys Gly Gly Gln Ala Lys Ile Lys Thr Asp
225                 230                 235                 240
Gly Asp Val Lys Ser Phe Asp Ile Asp Leu Ala Phe Phe Asp Ile Pro
                  245                 250                 255
Asn Ser Gly Ala Gly Asn Gly Thr Asn Val Asn Asp Asp Pro Asp Met
             260                 265                 270
Val Met Tyr Thr Glu Asn Val Asn Leu Glu Thr Pro Asp Thr His Ile
         275                 280                 285
Val Tyr Lys Pro Gly Thr Ser Asp Asp Ser Ser Lys Val Asn Leu Cys
     290                 295                 300
Gln Gln Ser Met Pro Asn Arg Pro Asn Tyr Ile Gly Phe Arg Asp Asn
305                 310                 315                 320
Phe Ile Gly Leu Met Tyr Tyr Asn Ser Thr Gly Asn Met Gly Val Leu
                  325                 330                 335
Ala Gly Gln Ala Ser Gln Leu Asn Ala Val Val Asp Leu Gln Asp Arg
             340                 345                 350
Asn Thr Glu Leu Ser Tyr Gln Leu Leu Leu Asp Ser Leu Gly Asp Arg
         355                 360                 365
Thr Arg Tyr Phe Ser Met Trp Asn Gln Ala Val Asp Ser Tyr Asp Pro
     370                 375                 380
Asp Val Arg Ile Ile Glu Asn His Gly Val Glu Asp Glu Leu Pro Asn
385                 390                 395                 400
Tyr Cys Phe Pro Leu Asp Gly Ala Gly Thr Asn Ser Val Tyr Gln Gly
                  405                 410                 415
Val Lys Pro Lys Thr Asp Asn Gly Asn Asp Gln Trp Glu Thr Asp Ser
             420                 425                 430
Thr Val Ser Ser His Asn Gln Ile Cys Lys Gly Asn Ile Tyr Ala Met
         435                 440                 445
Glu Ile Asn Leu Gln Ala Asn Leu Trp Arg Ser Phe Leu Tyr Ser Asn
     450                 455                 460
Val Ala Leu Tyr Leu Pro Asp Ser Tyr Lys Tyr Thr Pro Ala Asn Ile
465                 470                 475                 480
Thr Leu Pro Thr Asn Thr Asn Thr Tyr Asp Tyr Met Asn Gly Arg Val
                  485                 490                 495
Val Pro Pro Ser Leu Val Asp Ala Tyr Ile Asn Ile Gly Ala Arg Trp
             500                 505                 510
Ser Leu Asp Pro Met Asp Asn Val Asn Pro Phe Asn His His Arg Asn
         515                 520                 525
Ala Gly Leu Arg Tyr Arg Ser Met Leu Leu Gly Asn Gly Arg Tyr Val
     530                 535                 540
Pro Phe His Ile Gln Val Pro Gln Lys Phe Phe Ala Ile Lys Ser Leu
545                 550                 555                 560
Leu Leu Leu Pro Gly Ser Tyr Thr Tyr Glu Trp Asn Phe Arg Lys Asp
                  565                 570                 575
Val Asn Met Ile Leu Gln Ser Ser Leu Gly Asn Asp Leu Arg Thr Asp
             580                 585                 590
Gly Ala Ser Ile Ser Phe Thr Ser Ile Asn Leu Tyr Ala Thr Phe Phe
```

```
        595                 600                 605
Pro Met Ala His Asn Thr Ala Ser Thr Leu Glu Ala Met Leu Arg Asn
    610                 615                 620
Asp Thr Asn Asp Gln Ser Phe Asn Asp Tyr Leu Ser Ala Ala Asn Met
625                 630                 635                 640
Leu Tyr Pro Ile Pro Ala Asn Ala Thr Asn Val Pro Ile Ser Ile Pro
                645                 650                 655
Ser Arg Asn Trp Ala Ala Phe Arg Gly Trp Ser Phe Thr Arg Leu Lys
            660                 665                 670
Thr Arg Glu Thr Pro Ser Leu Gly Ser Gly Phe Asp Pro Tyr Phe Val
        675                 680                 685
Tyr Ser Gly Ser Ile Pro Tyr Leu Asp Gly Thr Phe Tyr Leu Asn His
    690                 695                 700
Thr Phe Lys Lys Val Ser Ile Thr Phe Asp Ser Ser Val Ser Trp Pro
705                 710                 715                 720
Gly Asn Asp Arg Leu Leu Thr Pro Asn Glu Phe Glu Ile Lys Arg Thr
                725                 730                 735
Val Asp Gly Glu Gly Tyr Asn Val Ala Gln Cys Asn Met Thr Lys Asp
            740                 745                 750
Trp Phe Leu Val Gln Met Leu Ala His Tyr Asn Ile Gly Tyr Gln Gly
        755                 760                 765
Phe Tyr Val Pro Glu Gly Tyr Lys Asp Arg Met Tyr Ser Phe Phe Arg
    770                 775                 780
Asn Phe Gln Pro Met Ser Arg Gln Val Val Asp Glu Val Asn Tyr Lys
785                 790                 795                 800
Asp Tyr Gln Ala Val Thr Leu Ala Tyr Gln His Asn Asn Ser Gly Phe
                805                 810                 815
Val Gly Tyr Leu Ala Pro Thr Met Arg Gln Gly Gln Pro Tyr Pro Ala
            820                 825                 830
Asn Tyr Pro Tyr Pro Leu Ile Gly Lys Ser Ala Val Thr Ser Val Thr
        835                 840                 845
Gln Lys Lys Phe Leu Cys Asp Arg Val Met Trp Arg Ile Pro Phe Ser
    850                 855                 860
Ser Asn Phe Met Ser Met Gly Ala Leu Thr Asp Leu Gly Gln Asn Met
865                 870                 875                 880
Leu Tyr Ala Asn Ser Ala His Ala Leu Asp Met Asn Phe Glu Val Asp
                885                 890                 895
Pro Met Asp Glu Ser Thr Leu Leu Tyr Val Val Phe Glu Val Phe Asp
            900                 905                 910
Val Val Arg Val His Gln Pro His Arg Gly Val Ile Glu Ala Val Tyr
        915                 920                 925
Leu Arg Thr Pro Phe Ser Ala Gly Asn Ala Thr Thr
    930                 935                 940


<210> 89
<211> 940
<212> PRT
<213> Chimpanzee Adenovirus- ChAd 5 Hexon

<400> 89
Met Ala Thr Pro Ser Met Leu Pro Gln Trp Ala Tyr Met His Ile Ala
 1               5                  10                  15
Gly Gln Asp Ala Ser Glu Tyr Leu Ser Pro Gly Leu Val Gln Phe Ala
            20                  25                  30
```

```
Arg Ala Thr Asp Thr Tyr Phe Ser Leu Gly Asn Lys Phe Arg Asn Pro
        35                  40                  45
Thr Val Ala Pro Thr His Asp Val Thr Thr Asp Arg Ser Gln Arg Leu
    50                  55                  60
Thr Leu Arg Phe Val Pro Val Asp Arg Glu Asp Asn Thr Tyr Ser Tyr
65                  70                  75                  80
Lys Val Arg Tyr Thr Leu Ala Val Gly Asp Asn Arg Val Leu Asp Met
                85                  90                  95
Ala Ser Thr Tyr Phe Asp Ile Arg Gly Val Leu Asp Arg Gly Pro Ser
            100                 105                 110
Phe Lys Pro Tyr Ser Gly Thr Ala Tyr Asn Ser Leu Ala Pro Lys Gly
        115                 120                 125
Ala Pro Asn Ser Ser Gln Trp Glu Gln Lys Lys Thr Gly Asn Asn Ala
    130                 135                 140
Asn Gly Asp Thr Glu Asn Val Thr Tyr Gly Val Ala Ala Met Gly Gly
145                 150                 155                 160
Ile Asp Ile Asp Lys Asn Gly Leu Gln Ile Gly Thr Asp Asp Thr Lys
                165                 170                 175
Asp Asp Asp Asn Glu Ile Tyr Ala Asp Lys Thr Tyr Gln Pro Glu Pro
            180                 185                 190
Gln Ile Gly Glu Glu Asn Trp Gln Glu Thr Tyr Ser Tyr Tyr Gly Gly
        195                 200                 205
Arg Ala Leu Lys Lys Asp Thr Lys Met Lys Pro Cys Tyr Gly Ser Phe
    210                 215                 220
Ala Arg Pro Thr Asn Val Lys Gly Gly Gln Ala Lys Ile Lys Thr Asp
225                 230                 235                 240
Gly Asp Val Lys Ser Phe Asp Ile Asp Leu Ala Phe Phe Asp Ile Pro
                245                 250                 255
Asn Ser Gly Ala Gly Asn Gly Thr Asn Val Asn Asp Asp Pro Asp Met
            260                 265                 270
Val Met Tyr Thr Glu Asn Val Asn Leu Glu Thr Pro Asp Thr His Ile
        275                 280                 285
Val Tyr Lys Pro Gly Thr Ser Asp Asp Ser Ser Lys Val Asn Leu Cys
    290                 295                 300
Gln Gln Ser Met Pro Asn Arg Pro Asn Tyr Ile Gly Phe Arg Asp Asn
305                 310                 315                 320
Phe Ile Gly Leu Met Tyr Tyr Asn Ser Thr Gly Asn Met Gly Val Leu
                325                 330                 335
Ala Gly Gln Ala Ser Gln Leu Asn Ala Val Val Asp Leu Gln Asp Arg
            340                 345                 350
Asn Thr Glu Leu Ser Tyr Gln Leu Leu Leu Asp Ser Leu Gly Asp Arg
        355                 360                 365
Thr Arg Tyr Phe Ser Met Trp Asn Gln Ala Val Asp Ser Tyr Asp Pro
    370                 375                 380
Asp Val Arg Ile Ile Glu Asn His Gly Val Glu Asp Glu Leu Pro Asn
385                 390                 395                 400
Tyr Cys Phe Pro Leu Asp Gly Ala Gly Thr Asn Ser Val Tyr Gln Gly
                405                 410                 415
Val Lys Pro Lys Thr Asp Asn Gly Asn Asp Gln Trp Glu Thr Asp Ser
            420                 425                 430
Thr Val Ser Ser His Asn Gln Ile Cys Lys Gly Asn Ile Tyr Ala Met
        435                 440                 445
Glu Ile Asn Leu Gln Ala Asn Leu Trp Arg Ser Phe Leu Tyr Ser Asn
    450                 455                 460
Val Ala Leu Tyr Leu Pro Asp Ser Tyr Lys Tyr Thr Pro Ala Asn Ile
```

```
465                 470                 475                 480
Thr Leu Pro Thr Asn Thr Asn Thr Tyr Asp Tyr Met Asn Gly Arg Val
                485                 490                 495
Val Pro Pro Ser Leu Val Asp Ala Tyr Ile Asn Ile Gly Ala Arg Trp
            500                 505                 510
Ser Leu Asp Pro Met Asp Asn Val Asn Pro Phe Asn His His Arg Asn
        515                 520                 525
Ala Gly Leu Arg Tyr Arg Ser Met Leu Leu Gly Asn Gly Arg Tyr Val
    530                 535                 540
Pro Phe His Ile Gln Val Pro Gln Lys Phe Phe Ala Ile Lys Ser Leu
545                 550                 555                 560
Leu Leu Leu Pro Gly Ser Tyr Thr Tyr Glu Trp Asn Phe Arg Lys Asp
                565                 570                 575
Val Asn Met Ile Leu Gln Ser Ser Leu Gly Asn Asp Leu Arg Thr Asp
            580                 585                 590
Gly Ala Ser Ile Ser Phe Thr Ser Ile Asn Leu Tyr Ala Thr Phe Phe
        595                 600                 605
Pro Met Ala His Asn Thr Ala Ser Thr Leu Glu Ala Met Leu Arg Asn
    610                 615                 620
Asp Thr Asn Asp Gln Ser Phe Asn Asp Tyr Leu Ser Ala Ala Asn Met
625                 630                 635                 640
Leu Tyr Pro Ile Pro Ala Asn Ala Thr Asn Val Pro Ile Ser Ile Pro
                645                 650                 655
Ser Arg Asn Trp Ala Ala Phe Arg Gly Trp Ser Phe Thr Arg Leu Lys
            660                 665                 670
Thr Arg Glu Thr Pro Ser Leu Gly Ser Gly Phe Asp Pro Tyr Phe Val
        675                 680                 685
Tyr Ser Gly Ser Ile Pro Tyr Leu Asp Gly Thr Phe Tyr Leu Asn His
    690                 695                 700
Thr Phe Lys Lys Val Ser Ile Thr Phe Asp Ser Ser Val Ser Trp Pro
705                 710                 715                 720
Gly Asn Asp Arg Leu Leu Thr Pro Asn Glu Phe Glu Ile Lys Arg Thr
                725                 730                 735
Val Asp Gly Glu Gly Tyr Asn Val Ala Gln Cys Asn Met Thr Lys Asp
            740                 745                 750
Trp Phe Leu Val Gln Met Leu Ala His Tyr Asn Ile Gly Tyr Gln Gly
        755                 760                 765
Phe Tyr Val Pro Glu Gly Tyr Lys Asp Arg Met Tyr Ser Phe Phe Arg
    770                 775                 780
Asn Phe Gln Pro Met Ser Arg Gln Val Val Asp Glu Val Asn Tyr Lys
785                 790                 795                 800
Asp Tyr Gln Ala Val Thr Leu Ala Tyr Gln His Asn Asn Ser Gly Phe
                805                 810                 815
Val Gly Tyr Leu Ala Pro Thr Met Arg Gln Gly Gln Pro Tyr Pro Ala
            820                 825                 830
Asn Tyr Pro Tyr Pro Leu Ile Gly Lys Ser Ala Val Ala Ser Val Thr
        835                 840                 845
Gln Lys Lys Phe Leu Cys Asp Arg Val Met Trp Arg Ile Pro Phe Ser
    850                 855                 860
Ser Asn Phe Met Ser Met Gly Ala Leu Thr Asp Leu Gly Gln Asn Met
865                 870                 875                 880
Leu Tyr Ala Asn Ser Ala His Ala Leu Asp Met Asn Phe Glu Val Asp
                885                 890                 895
Pro Met Asp Glu Ser Thr Leu Leu Tyr Val Val Phe Glu Val Phe Asp
            900                 905                 910
```

```
Val Val Arg Val His Gln Pro His Arg Gly Val Ile Glu Ala Val Tyr
        915                 920                 925
Leu Arg Thr Pro Phe Ser Ala Gly Lys Ala Thr Thr
    930                 935                 940
```

<210> 90
<211> 940
<212> PRT
<213> Chimpanzee Adenovirus- ChAd 7 Hexon

<400> 90

```
Met Ala Thr Pro Ser Met Leu Pro Gln Trp Ala Tyr Met His Ile Ala
 1               5                  10                  15
Gly Gln Asp Ala Ser Glu Tyr Leu Ser Pro Gly Leu Val Gln Phe Ala
            20                  25                  30
Arg Ala Thr Asp Thr Tyr Phe Ser Leu Gly Asn Lys Phe Arg Asn Pro
        35                  40                  45
Thr Val Ala Pro Thr His Asp Val Thr Thr Asp Arg Ser Gln Arg Leu
    50                  55                  60
Thr Leu Arg Phe Val Pro Val Asp Arg Glu Asp Asn Thr Tyr Ser Tyr
65                  70                  75                  80
Lys Val Arg Tyr Thr Leu Ala Val Gly Asp Asn Arg Val Leu Asp Met
                85                  90                  95
Ala Ser Thr Tyr Phe Asp Ile Arg Gly Val Leu Asp Arg Gly Pro Ser
            100                 105                 110
Phe Lys Pro Tyr Ser Gly Thr Ala Tyr Asn Ser Leu Ala Pro Lys Gly
        115                 120                 125
Ala Pro Asn Ser Ser Gln Trp Glu Gln Lys Lys Thr Gly Lys Asn Ala
    130                 135                 140
Asn Gly Asp Thr Glu Asn Val Thr Tyr Gly Val Ala Ala Met Gly Gly
145                 150                 155                 160
Ile Asp Ile Asp Lys Asn Gly Leu Gln Ile Gly Thr Asp Asp Thr Lys
                165                 170                 175
Asp Gly Asp Asn Glu Ile Tyr Ala Asp Lys Thr Tyr Gln Pro Glu Pro
            180                 185                 190
Gln Ile Gly Glu Glu Asn Trp Gln Glu Thr Tyr Ser Tyr Tyr Gly Gly
        195                 200                 205
Arg Ala Leu Lys Lys Asp Thr Lys Met Lys Pro Cys Tyr Gly Ser Phe
    210                 215                 220
Ala Arg Pro Thr Asn Val Lys Gly Gly Gln Ala Lys Ile Lys Thr Asp
225                 230                 235                 240
Gly Asp Val Lys Ser Phe Asp Ile Asp Leu Ala Phe Phe Asp Ile Pro
                245                 250                 255
Asn Ser Gly Ala Gly Asn Gly Thr Asn Val Asn Asp Asp Pro Asp Met
            260                 265                 270
Val Met Tyr Thr Glu Asn Val Asn Leu Glu Thr Pro Asp Thr His Ile
        275                 280                 285
Val Tyr Lys Pro Gly Thr Ser Asp Asp Ser Ser Glu Val Asn Leu Cys
    290                 295                 300
Gln Gln Ser Met Pro Asn Arg Pro Asn Tyr Ile Gly Phe Arg Asp Asn
305                 310                 315                 320
Phe Ile Gly Leu Met Tyr Tyr Asn Ser Thr Gly Asn Met Gly Val Leu
                325                 330                 335
Ala Gly Gln Ala Ser Gln Leu Asn Ala Val Val Asp Leu Gln Asp Arg
```

```
                340                 345                 350
Asn Thr Glu Leu Ser Tyr Gln Leu Leu Leu Asp Ser Leu Gly Asp Arg
        355                 360                 365
Thr Arg Tyr Phe Ser Met Trp Asn Gln Ala Val Asp Ser Tyr Asp Pro
    370                 375                 380
Asp Val Arg Ile Ile Glu Asn His Gly Val Glu Asp Glu Leu Pro Asn
385                 390                 395                 400
Tyr Cys Phe Pro Leu Asp Gly Ala Gly Thr Asn Ser Val Tyr Gln Gly
                405                 410                 415
Val Lys Pro Lys Thr Asp Asn Gly Asn Asp Gln Trp Glu Thr Asp Ser
            420                 425                 430
Thr Val Ser Ser His Asn Gln Ile Cys Lys Gly Asn Ile Tyr Ala Met
        435                 440                 445
Glu Ile Asn Leu Gln Ala Asn Leu Trp Arg Ser Phe Leu Tyr Ser Asn
    450                 455                 460
Val Ala Leu Tyr Leu Pro Asp Ser Tyr Lys Tyr Thr Pro Ala Asn Ile
465                 470                 475                 480
Thr Leu Pro Thr Asn Thr Asn Thr Tyr Asp Tyr Met Asn Gly Arg Val
                485                 490                 495
Val Pro Pro Ser Leu Val Asp Ala Tyr Ile Asn Ile Gly Ala Arg Trp
            500                 505                 510
Ser Leu Asp Pro Met Asp Asn Val Asn Pro Phe Asn His His Arg Asn
        515                 520                 525
Ala Gly Leu Arg Tyr Arg Ser Met Leu Leu Gly Asn Gly Arg Tyr Val
    530                 535                 540
Pro Phe His Ile Gln Val Pro Gln Lys Phe Phe Ala Ile Lys Ser Leu
545                 550                 555                 560
Leu Leu Leu Pro Gly Ser Tyr Thr Tyr Glu Trp Asn Phe Arg Lys Asp
                565                 570                 575
Val Asn Met Ile Leu Gln Ser Ser Leu Gly Asn Asp Leu Arg Thr Asp
            580                 585                 590
Gly Ala Ser Ile Ser Phe Thr Ser Ile Asn Leu Tyr Ala Thr Phe Phe
        595                 600                 605
Pro Met Ala His Asn Thr Ala Ser Thr Leu Glu Ala Met Leu Arg Asn
    610                 615                 620
Asp Thr Asn Asp Gln Ser Phe Asn Asp Tyr Leu Ser Ala Ala Asn Met
625                 630                 635                 640
Leu Tyr Pro Ile Pro Ala Asn Ala Thr Asn Val Pro Ile Ser Ile Pro
                645                 650                 655
Ser Arg Asn Trp Ala Ala Phe Arg Gly Trp Ser Phe Thr Arg Leu Lys
            660                 665                 670
Thr Lys Glu Thr Pro Ser Leu Gly Ser Gly Phe Asp Pro Tyr Phe Val
        675                 680                 685
Tyr Ser Gly Ser Ile Pro Tyr Leu Asp Gly Thr Phe Tyr Leu Asn His
    690                 695                 700
Thr Phe Lys Lys Val Ser Ile Thr Phe Asp Ser Ser Val Ser Trp Pro
705                 710                 715                 720
Gly Asn Asp Arg Leu Leu Thr Pro Asn Glu Phe Glu Ile Lys Arg Thr
                725                 730                 735
Val Asp Gly Glu Gly Tyr Asn Val Ala Gln Cys Asn Met Thr Lys Asp
            740                 745                 750
Trp Phe Leu Val Gln Met Leu Ala His Tyr Asn Ile Gly Tyr Gln Gly
        755                 760                 765
Phe Tyr Val Pro Glu Gly Tyr Lys Asp Arg Met Tyr Ser Phe Phe Arg
    770                 775                 780
```

```
Asn Phe Gln Pro Met Ser Arg Gln Val Val Asp Glu Val Asn Tyr Lys
785                 790                 795                 800
Asp Tyr Gln Ala Val Thr Leu Ala Tyr Gln His Asn Asn Ser Gly Phe
                805                 810                 815
Val Gly Tyr Leu Ala Pro Thr Met Arg Gln Gly Gln Pro Tyr Pro Ala
            820                 825                 830
Asn Tyr Pro Tyr Pro Leu Ile Gly Lys Ser Ala Val Thr Ser Val Thr
        835                 840                 845
Gln Lys Lys Phe Leu Cys Asp Arg Val Met Trp Arg Ile Pro Phe Ser
    850                 855                 860
Ser Asn Phe Met Ser Met Gly Ala Leu Thr Asp Leu Gly Gln Asn Met
865                 870                 875                 880
Leu Tyr Ala Asn Ser Ala His Ala Leu Asp Met Asn Phe Glu Val Asp
                885                 890                 895
Pro Met Asp Glu Ser Thr Leu Leu Tyr Val Val Phe Glu Val Phe Asp
            900                 905                 910
Val Val Arg Val His Gln Pro His Arg Gly Val Ile Glu Ala Val Tyr
        915                 920                 925
Leu Arg Thr Pro Phe Ser Ala Gly Asn Ala Thr Thr
    930                 935                 940


<210> 91
<211> 930
<212> PRT
<213> Chimpanzee Adenovirus- ChAd 9 Hexon

<400> 91
Met Ala Thr Pro Ser Met Leu Pro Gln Trp Ala Tyr Met His Ile Ala
 1                5                  10                  15
Gly Gln Asp Ala Ser Glu Tyr Leu Ser Pro Gly Leu Val Gln Phe Ala
            20                  25                  30
Arg Ala Thr Asp Thr Tyr Phe Ser Leu Gly Asn Lys Phe Arg Asn Pro
        35                  40                  45
Thr Val Ala Pro Thr His Asp Val Thr Thr Asp Arg Ser Gln Arg Leu
    50                  55                  60
Thr Leu Arg Phe Val Pro Val Asp Arg Glu Asp Asn Thr Tyr Ser Tyr
65                  70                  75                  80
Lys Val Arg Tyr Thr Leu Ala Val Gly Asp Asn Arg Val Leu Asp Met
                85                  90                  95
Ala Ser Thr Tyr Phe Asp Ile Arg Gly Val Leu Asp Arg Gly Pro Ser
            100                 105                 110
Phe Lys Pro Tyr Ser Gly Thr Ala Tyr Asn Ser Leu Ala Pro Lys Gly
        115                 120                 125
Ala Pro Asn Thr Cys Gln Trp Thr Tyr Thr Asp Asn Gln Thr Glu Lys
    130                 135                 140
Thr Ala Thr Tyr Gly Asn Ala Pro Val Glu Gly Ile Asn Ile Thr Lys
145                 150                 155                 160
Asp Gly Ile Gln Leu Gly Thr Asp Ser Asp Gly Gln Ala Ile Tyr Ala
                165                 170                 175
Asp Glu Thr Tyr Gln Pro Glu Pro Gln Val Gly Asp Pro Glu Trp His
            180                 185                 190
Asp Thr Thr Gly Thr Glu Glu Lys Tyr Gly Gly Arg Ala Leu Lys Pro
        195                 200                 205
Ala Thr Asp Met Lys Pro Cys Tyr Gly Ser Phe Ala Lys Pro Thr Asn
```

```
    210                 215                 220
Val Lys Gly Gly Gln Ala Lys Ser Arg Thr Lys Thr Asp Gly Thr Thr
225                 230                 235                 240
Glu Pro Asp Ile Asp Met Ala Phe Phe Asp Gly Arg Asn Ala Thr Thr
                245                 250                 255
Ala Gly Leu Thr Pro Glu Ile Val Leu Tyr Thr Glu Asn Val Asp Leu
            260                 265                 270
Glu Thr Pro Asp Thr His Ile Val Tyr Lys Ala Gly Thr Asp Asp Ser
        275                 280                 285
Ser Ser Ser Ile Asn Leu Gly Gln Gln Ser Met Pro Asn Arg Pro Asn
    290                 295                 300
Tyr Ile Gly Phe Arg Asp Asn Phe Ile Gly Leu Met Tyr Tyr Asn Ser
305                 310                 315                 320
Thr Gly Asn Met Gly Val Leu Ala Gly Gln Ala Ser Gln Leu Asn Ala
                325                 330                 335
Val Val Asp Leu Gln Asp Arg Asn Thr Glu Leu Ser Tyr Gln Leu Leu
            340                 345                 350
Leu Asp Ser Leu Gly Asp Arg Thr Arg Tyr Phe Ser Met Trp Asn Gln
        355                 360                 365
Ala Val Asp Ser Tyr Asp Pro Asp Val Arg Ile Ile Glu Asn His Gly
    370                 375                 380
Val Glu Asp Glu Leu Pro Asn Tyr Cys Phe Pro Leu Asn Ala Val Gly
385                 390                 395                 400
Arg Thr Asn Ser Tyr Gln Gly Ile Lys Pro Asn Gly Gly Asp Pro Ala
                405                 410                 415
Thr Trp Ala Lys Asp Glu Ser Val Asn Asp Ser Asn Glu Leu Gly Lys
            420                 425                 430
Gly Asn Pro Phe Ala Met Glu Ile Asn Ile Gln Ala Asn Leu Trp Arg
        435                 440                 445
Asn Phe Leu Tyr Ala Asn Val Ala Leu Tyr Leu Pro Asp Ser Tyr Lys
    450                 455                 460
Tyr Thr Pro Ala Asn Ile Thr Leu Pro Ala Asn Thr Asn Thr Tyr Asp
465                 470                 475                 480
Tyr Met Asn Gly Arg Val Val Ala Pro Ser Leu Val Asp Ala Tyr Ile
                485                 490                 495
Asn Ile Gly Ala Arg Trp Ser Leu Asp Pro Met Asp Asn Val Asn Pro
            500                 505                 510
Phe Asn His His Arg Asn Ala Gly Leu Arg Tyr Arg Ser Met Leu Leu
        515                 520                 525
Gly Asn Gly Arg Tyr Val Pro Phe His Ile Gln Val Pro Gln Lys Phe
    530                 535                 540
Phe Ala Ile Lys Ser Leu Leu Leu Leu Pro Gly Ser Tyr Thr Tyr Glu
545                 550                 555                 560
Trp Asn Phe Arg Lys Asp Val Asn Met Ile Leu Gln Ser Ser Leu Gly
                565                 570                 575
Asn Asp Leu Arg Thr Asp Gly Ala Ser Ile Ala Phe Thr Ser Ile Asn
            580                 585                 590
Leu Tyr Ala Thr Phe Phe Pro Met Ala His Asn Thr Ala Ser Thr Leu
        595                 600                 605
Glu Ala Met Leu Arg Asn Asp Thr Asn Asp Gln Ser Phe Asn Asp Tyr
    610                 615                 620
Leu Ser Ala Ala Asn Met Leu Tyr Pro Ile Pro Ala Asn Ala Thr Asn
625                 630                 635                 640
Val Pro Ile Ser Ile Pro Ser Arg Asn Trp Ala Ala Phe Arg Gly Trp
                645                 650                 655
```

```
Ser Phe Thr Arg Leu Lys Thr Arg Glu Thr Pro Ser Leu Gly Ser Gly
                660                 665                 670
Phe Asp Pro Tyr Phe Val Tyr Ser Gly Ser Ile Pro Tyr Leu Asp Gly
        675                 680                 685
Thr Phe Tyr Leu Asn His Thr Phe Lys Lys Val Ser Ile Thr Phe Asp
    690                 695                 700
Ser Ser Val Ser Trp Pro Gly Asn Asp Arg Leu Leu Thr Pro Asn Glu
705                 710                 715                 720
Phe Glu Ile Lys Arg Thr Val Asp Gly Glu Gly Tyr Asn Val Ala Gln
                725                 730                 735
Cys Asn Met Thr Lys Asp Trp Phe Leu Val Gln Met Leu Ala His Tyr
            740                 745                 750
Asn Ile Gly Tyr Gln Gly Phe Tyr Val Pro Glu Gly Tyr Lys Asp Arg
        755                 760                 765
Met Tyr Ser Phe Phe Arg Asn Phe Gln Pro Met Ser Arg Gln Val Val
    770                 775                 780
Asp Glu Val Asn Tyr Lys Asp Tyr Gln Ala Val Thr Leu Ala Tyr Gln
785                 790                 795                 800
His Asn Asn Ser Gly Phe Val Gly Tyr Leu Ala Pro Thr Met Arg Gln
                805                 810                 815
Gly Gln Pro Tyr Pro Ala Asn Tyr Pro Tyr Pro Leu Ile Gly Lys Ser
            820                 825                 830
Ala Val Ala Ser Val Thr Gln Lys Lys Phe Leu Cys Asp Arg Val Met
        835                 840                 845
Trp Arg Ile Pro Phe Ser Ser Asn Phe Met Ser Met Gly Ala Leu Thr
    850                 855                 860
Asp Leu Gly Gln Asn Met Leu Tyr Ala Asn Ser Ala His Ala Leu Asp
865                 870                 875                 880
Met Asn Phe Glu Val Asp Pro Met Asp Glu Ser Thr Leu Leu Tyr Val
                885                 890                 895
Val Phe Glu Val Phe Asp Val Val Arg Val His Gln Pro His Arg Gly
            900                 905                 910
Val Ile Glu Ala Val Tyr Leu Arg Thr Pro Phe Ser Ala Gly Asn Ala
        915                 920                 925
Thr Thr
    930
```

<210> 92
<211> 930
<212> PRT
<213> Chimpanzee Adenovirus- ChAd 10 Hexon

<400> 92

```
Met Ala Thr Pro Ser Met Leu Pro Gln Trp Ala Tyr Met His Ile Ala
 1                5                  10                  15
Gly Gln Asp Ala Ser Glu Tyr Leu Ser Pro Gly Leu Val Gln Phe Ala
            20                  25                  30
Arg Ala Thr Asp Thr Tyr Phe Ser Leu Gly Asn Lys Phe Arg Asn Pro
        35                  40                  45
Thr Val Ala Pro Thr His Asp Val Thr Thr Asp Arg Ser Gln Arg Leu
    50                  55                  60
Thr Leu Arg Phe Val Pro Val Asp Arg Glu Asp Asn Thr Tyr Ser Tyr
65                  70                  75                  80
Lys Val Arg Tyr Thr Leu Ala Val Gly Asp Asn Arg Val Leu Asp Met
```

```
                85                  90                  95
Ala Ser Thr Tyr Phe Asp Ile Arg Gly Val Leu Asp Arg Gly Pro Ser
            100                 105                 110
Phe Lys Pro Tyr Ser Gly Thr Ala Tyr Asn Ser Leu Ala Pro Lys Gly
        115                 120                 125
Ala Pro Asn Thr Cys Gln Trp Thr Tyr Thr Asp Asn Gln Thr Glu Lys
    130                 135                 140
Thr Ala Thr Tyr Gly Asn Ala Pro Val Gln Gly Ile Ser Ile Thr Lys
145                 150                 155                 160
Asp Gly Ile Gln Leu Gly Thr Asp Thr Asp Asp Gln Pro Ile Tyr Ala
                165                 170                 175
Asp Lys Thr Tyr Gln Pro Glu Pro Gln Val Gly Asp Ala Glu Trp His
            180                 185                 190
Asp Ile Thr Gly Thr Asp Glu Lys Tyr Gly Gly Arg Ala Leu Lys Pro
        195                 200                 205
Asp Thr Lys Met Lys Pro Cys Tyr Gly Ser Phe Ala Lys Pro Thr Asn
    210                 215                 220
Lys Glu Gly Gly Gln Ala Asn Val Lys Thr Glu Thr Gly Gly Thr Lys
225                 230                 235                 240
Glu Tyr Asp Ile Asp Met Ala Phe Phe Asp Asn Arg Ser Ala Ala Ala
                245                 250                 255
Ala Gly Leu Ala Pro Glu Ile Val Leu Tyr Thr Glu Asn Val Asp Leu
            260                 265                 270
Glu Thr Pro Asp Thr His Ile Val Tyr Lys Ala Gly Thr Asp Asp Ser
        275                 280                 285
Ser Ser Ser Ile Asn Leu Gly Gln Gln Ser Met Pro Asn Arg Pro Asn
    290                 295                 300
Tyr Ile Gly Phe Arg Asp Asn Phe Ile Gly Leu Met Tyr Tyr Asn Ser
305                 310                 315                 320
Thr Gly Asn Met Gly Val Leu Ala Gly Gln Ala Ser Gln Leu Asn Ala
                325                 330                 335
Val Val Asp Leu Gln Asp Arg Asn Thr Glu Leu Ser Tyr Gln Leu Leu
            340                 345                 350
Leu Asp Ser Leu Gly Asp Arg Thr Arg Tyr Phe Ser Met Trp Asn Gln
        355                 360                 365
Ala Val Asp Ser Tyr Asp Pro Asp Val Arg Ile Ile Glu Asn His Gly
    370                 375                 380
Val Glu Asp Glu Leu Pro Asn Tyr Cys Phe Pro Leu Asn Ala Val Gly
385                 390                 395                 400
Arg Thr Asp Thr Tyr Gln Gly Ile Lys Ala Asn Gly Ala Asp Gln Thr
                405                 410                 415
Thr Trp Thr Lys Asp Asp Thr Val Asn Asp Ala Asn Glu Leu Gly Lys
            420                 425                 430
Gly Asn Pro Phe Ala Met Glu Ile Asn Ile Gln Ala Asn Leu Trp Arg
        435                 440                 445
Asn Phe Leu Tyr Ala Asn Val Ala Leu Tyr Leu Pro Asp Ser Tyr Lys
    450                 455                 460
Tyr Thr Pro Ala Asn Ile Thr Leu Pro Thr Asn Thr Asn Thr Tyr Asp
465                 470                 475                 480
Tyr Met Asn Gly Arg Val Val Ala Pro Ser Leu Val Asp Ala Tyr Ile
                485                 490                 495
Asn Ile Gly Ala Arg Trp Ser Leu Asp Pro Met Asp Asn Val Asn Pro
            500                 505                 510
Phe Asn His His Arg Asn Ala Gly Leu Arg Tyr Arg Ser Met Leu Leu
        515                 520                 525
```

```
Gly Asn Gly Arg Tyr Val Pro Phe His Ile Gln Val Pro Gln Lys Phe
    530                 535                 540
Phe Ala Ile Lys Ser Leu Leu Leu Leu Pro Gly Ser Tyr Thr Tyr Glu
545                 550                 555                 560
Trp Asn Phe Arg Lys Asp Val Asn Met Ile Leu Gln Ser Ser Leu Gly
                565                 570                 575
Asn Asp Leu Arg Thr Asp Gly Ala Ser Ile Ala Phe Thr Ser Ile Asn
            580                 585                 590
Leu Tyr Ala Thr Phe Phe Pro Met Ala His Asn Thr Ala Ser Thr Leu
        595                 600                 605
Glu Ala Met Leu Arg Asn Asp Thr Asn Asp Gln Ser Phe Asn Asp Tyr
    610                 615                 620
Leu Ser Ala Ala Asn Met Leu Tyr Pro Ile Pro Ala Asn Ala Thr Asn
625                 630                 635                 640
Val Pro Ile Ser Ile Pro Ser Arg Asn Trp Ala Ala Phe Arg Gly Trp
                645                 650                 655
Ser Phe Thr Arg Leu Lys Thr Arg Glu Thr Pro Ser Leu Gly Ser Gly
            660                 665                 670
Phe Asp Pro Tyr Phe Val Tyr Ser Gly Ser Ile Pro Tyr Leu Asp Gly
        675                 680                 685
Thr Phe Tyr Leu Asn His Thr Phe Lys Lys Val Ser Ile Thr Phe Asp
    690                 695                 700
Ser Ser Val Ser Trp Pro Gly Asn Asp Arg Leu Leu Thr Pro Asn Glu
705                 710                 715                 720
Phe Glu Ile Lys Arg Thr Val Asp Gly Glu Gly Tyr Asn Val Ala Gln
                725                 730                 735
Cys Asn Met Thr Lys Asp Trp Phe Leu Val Gln Met Leu Ala His Tyr
            740                 745                 750
Asn Ile Gly Tyr Gln Gly Phe Tyr Val Pro Glu Gly Tyr Lys Asp Arg
        755                 760                 765
Met Tyr Ser Phe Phe Arg Asn Phe Gln Pro Met Ser Arg Gln Val Val
    770                 775                 780
Asp Glu Val Asn Tyr Lys Asp Tyr Gln Ala Val Thr Leu Ala Tyr Gln
785                 790                 795                 800
His Asn Asn Ser Gly Phe Val Gly Tyr Leu Ala Pro Thr Met Arg Gln
                805                 810                 815
Gly Gln Pro Tyr Pro Ala Asn Tyr Pro Tyr Pro Leu Ile Gly Lys Ser
            820                 825                 830
Ala Val Ala Ser Val Thr Gln Lys Lys Phe Leu Cys Asp Arg Val Met
        835                 840                 845
Trp Arg Ile Pro Phe Ser Ser Asn Phe Met Ser Met Gly Ala Leu Thr
    850                 855                 860
Asp Leu Gly Gln Asn Met Leu Tyr Ala Asn Ser Ala His Ala Leu Asp
865                 870                 875                 880
Met Asn Phe Glu Val Asp Pro Met Asp Glu Ser Thr Leu Leu Tyr Val
                885                 890                 895
Val Phe Glu Val Phe Asp Val Val Arg Val His Gln Pro His Arg Gly
            900                 905                 910
Val Ile Glu Ala Val Tyr Leu Arg Thr Pro Phe Ser Ala Gly Asn Ala
        915                 920                 925
Thr Thr
    930
```

<210> 93

<211> 960
<212> PRT
<213> Chimpanzee Adenovirus- ChAd 11 Hexon

<400> 93

```
Met Ala Thr Pro Ser Met Met Pro Gln Trp Ser Tyr Met His Ile Ser
 1               5                  10                  15
Gly Gln Asp Ala Ser Glu Tyr Leu Ser Pro Gly Leu Val Gln Phe Ala
            20                  25                  30
Arg Ala Thr Glu Ser Tyr Phe Ser Leu Ser Asn Lys Phe Arg Asn Pro
        35                  40                  45
Thr Val Ala Pro Thr His Asp Val Thr Thr Asp Arg Ser Gln Arg Leu
    50                  55                  60
Thr Leu Arg Phe Ile Pro Val Asp Arg Glu Asp Thr Ala Tyr Ser Tyr
65                  70                  75                  80
Lys Ala Arg Phe Thr Leu Ala Val Gly Asp Asn Arg Val Leu Asp Met
                85                  90                  95
Ala Ser Thr Tyr Phe Asp Ile Arg Gly Val Leu Asp Arg Gly Pro Thr
            100                 105                 110
Phe Lys Pro Tyr Ser Gly Thr Ala Tyr Asn Ser Leu Ala Pro Lys Gly
        115                 120                 125
Ala Pro Asn Ser Cys Glu Trp Glu Gln Glu Glu Thr Gln Ala Val Glu
    130                 135                 140
Glu Ala Ala Glu Glu Glu Glu Glu Asp Ala Asp Gly Gln Ala Glu Glu
145                 150                 155                 160
Glu Gln Ala Ala Thr Lys Lys Thr His Val Tyr Ala Gln Ala Pro Leu
                165                 170                 175
Ser Gly Glu Lys Ile Ser Lys Asp Gly Leu Gln Ile Gly Thr Asp Ala
            180                 185                 190
Thr Ala Thr Glu Gln Lys Pro Ile Tyr Ala Asp Pro Thr Phe Gln Pro
        195                 200                 205
Glu Pro Gln Ile Gly Glu Ser Gln Trp Asn Glu Ala Asp Ala Thr Val
    210                 215                 220
Ala Gly Gly Arg Val Leu Lys Lys Thr Thr Pro Met Lys Pro Cys Tyr
225                 230                 235                 240
Gly Ser Tyr Ala Arg Pro Thr Asn Ala Asn Gly Gly Gln Gly Val Leu
                245                 250                 255
Ala Ala Asn Ala Gln Gly Gln Leu Glu Ser Gln Val Glu Met Gln Phe
            260                 265                 270
Phe Ser Thr Ser Glu Asn Ala Arg Asn Glu Ala Asn Asn Ile Gln Pro
        275                 280                 285
Lys Leu Val Leu Tyr Ser Glu Asp Val His Met Glu Thr Pro Asp Thr
    290                 295                 300
His Leu Ser Tyr Lys Pro Thr Lys Ser Asp Asp Asn Ser Lys Val Met
305                 310                 315                 320
Leu Gly Gln Gln Ala Met Pro Asn Arg Pro Asn Tyr Ile Gly Phe Arg
                325                 330                 335
Asp Asn Phe Ile Gly Leu Met Tyr Tyr Asn Ser Thr Gly Asn Met Gly
            340                 345                 350
Val Leu Ala Gly Gln Ala Ser Gln Leu Asn Ala Val Val Asp Leu Gln
        355                 360                 365
Asp Arg Asn Thr Glu Leu Ser Tyr Gln Leu Leu Leu Asp Ser Met Gly
    370                 375                 380
Asp Arg Thr Arg Tyr Phe Ser Met Trp Asn Gln Ala Val Asp Ser Tyr
385                 390                 395                 400
```

```
Asp Pro Asp Val Arg Ile Ile Glu Asn His Gly Thr Glu Asp Glu Leu
                405                 410                 415
Pro Asn Tyr Cys Phe Pro Leu Gly Gly Ile Gly Val Thr Asp Thr Tyr
            420                 425                 430
Gln Ala Val Lys Thr Asn Asn Gly Asn Asn Gly Gly Gln Val Thr Trp
        435                 440                 445
Thr Lys Asp Glu Thr Phe Ala Glu Arg Asn Glu Ile Gly Val Gly Asn
    450                 455                 460
Asn Phe Ala Met Glu Ile Asn Leu Asn Ala Asn Leu Trp Arg Asn Phe
465                 470                 475                 480
Leu Tyr Ser Asn Val Ala Leu Tyr Leu Pro Asp Lys Leu Lys Tyr Asn
                485                 490                 495
Pro Ser Asn Val Asp Ile Ser Asp Asn Pro Asn Thr Tyr Asp Tyr Met
            500                 505                 510
Asn Lys Arg Val Val Ala Pro Gly Leu Val Asp Cys Tyr Ile Asn Leu
        515                 520                 525
Gly Ala Arg Trp Ser Leu Asp Tyr Met Asp Asn Val Asn Pro Phe Asn
    530                 535                 540
His His Arg Asn Ala Gly Leu Arg Tyr Arg Ser Met Leu Leu Gly Asn
545                 550                 555                 560
Gly Arg Tyr Val Pro Phe His Ile Gln Val Pro Gln Lys Phe Phe Ala
                565                 570                 575
Ile Lys Asn Leu Leu Leu Leu Pro Gly Ser Tyr Thr Tyr Glu Trp Asn
            580                 585                 590
Phe Arg Lys Asp Val Asn Met Val Leu Gln Ser Ser Leu Gly Asn Asp
        595                 600                 605
Leu Arg Val Asp Gly Ala Ser Ile Lys Phe Glu Ser Ile Cys Leu Tyr
    610                 615                 620
Ala Thr Phe Phe Pro Met Ala His Asn Thr Ala Ser Thr Leu Glu Ala
625                 630                 635                 640
Met Leu Arg Asn Asp Thr Asn Asp Gln Ser Phe Asn Asp Tyr Leu Ser
                645                 650                 655
Ala Ala Asn Met Leu Tyr Pro Ile Pro Ala Asn Ala Thr Asn Val Pro
            660                 665                 670
Ile Ser Ile Pro Ser Arg Asn Trp Ala Ala Phe Arg Gly Trp Ala Phe
        675                 680                 685
Thr Arg Leu Lys Thr Lys Glu Thr Pro Ser Leu Gly Ser Gly Phe Asp
    690                 695                 700
Pro Tyr Tyr Thr Tyr Ser Gly Ser Ile Pro Tyr Leu Asp Gly Thr Phe
705                 710                 715                 720
Tyr Leu Asn His Thr Phe Lys Lys Val Ser Val Thr Phe Asp Ser Ser
                725                 730                 735
Val Ser Trp Pro Gly Asn Asp Arg Leu Leu Thr Pro Asn Glu Phe Glu
            740                 745                 750
Ile Lys Arg Ser Val Asp Gly Glu Gly Tyr Asn Val Ala Gln Cys Asn
        755                 760                 765
Met Thr Lys Asp Trp Phe Leu Val Gln Met Leu Ala Asn Tyr Asn Ile
    770                 775                 780
Gly Tyr Gln Gly Phe Tyr Ile Pro Glu Ser Tyr Lys Asp Arg Met Tyr
785                 790                 795                 800
Ser Phe Phe Arg Asn Phe Gln Pro Met Ser Arg Gln Val Val Asp Gln
                805                 810                 815
Thr Lys Tyr Lys Asp Tyr Gln Glu Val Gly Ile Ile His Gln His Asn
            820                 825                 830
Asn Ser Gly Phe Val Gly Tyr Leu Ala Pro Thr Met Arg Glu Gly Gln
```

```
        835                 840                 845
Ala Tyr Pro Ala Asn Phe Pro Tyr Pro Leu Ile Gly Lys Thr Ala Val
    850                 855                 860
Asp Ser Ile Thr Gln Lys Lys Phe Leu Cys Asp Arg Thr Leu Trp Arg
865                 870                 875                 880
Ile Pro Phe Ser Ser Asn Phe Met Ser Met Gly Ala Leu Thr Asp Leu
                885                 890                 895
Gly Gln Asn Leu Leu Tyr Ala Asn Ser Ala His Ala Leu Asp Met Thr
            900                 905                 910
Phe Glu Val Asp Pro Met Asp Glu Pro Thr Leu Leu Tyr Val Leu Phe
        915                 920                 925
Glu Val Phe Asp Val Val Arg Val His Gln Pro His Arg Gly Val Ile
    930                 935                 940
Glu Thr Val Tyr Leu Arg Thr Pro Phe Ser Ala Gly Asn Ala Thr Thr
945                 950                 955                 960


<210> 94
<211> 944
<212> PRT
<213> Chimpanzee Adenovirus- ChAd 16 Hexon

<400> 94
Met Ala Thr Pro Ser Met Leu Pro Gln Trp Ala Tyr Met His Ile Ala
 1               5                  10                  15
Gly Gln Asp Ala Ser Glu Tyr Leu Ser Pro Gly Leu Val Gln Phe Ala
            20                  25                  30
Arg Ala Thr Asp Thr Tyr Phe Ser Leu Gly Asn Lys Phe Arg Asn Pro
        35                  40                  45
Thr Val Ala Pro Thr His Asp Val Thr Thr Asp Arg Ser Gln Arg Leu
    50                  55                  60
Thr Leu Arg Phe Val Pro Val Asp Arg Glu Asp Asn Thr Tyr Ser Tyr
65                  70                  75                  80
Lys Val Arg Tyr Thr Leu Ala Val Gly Asp Asn Arg Val Leu Asp Met
                85                  90                  95
Ala Ser Thr Tyr Phe Asp Ile Arg Gly Val Leu Asp Arg Gly Pro Ser
            100                 105                 110
Phe Lys Pro Tyr Ser Gly Thr Ala Tyr Asn Ser Leu Ala Pro Lys Gly
        115                 120                 125
Ala Pro Asn Ser Ser Gln Trp Glu Gln Thr Glu Asn Gly Gly Gly Gln
    130                 135                 140
Ala Thr Thr Lys Thr His Thr Tyr Gly Val Ala Pro Met Gly Gly Thr
145                 150                 155                 160
Asn Ile Thr Val Asp Gly Leu Gln Ile Gly Thr Asp Ala Thr Ala Asp
                165                 170                 175
Thr Glu Lys Pro Ile Tyr Ala Asp Lys Thr Phe Gln Pro Glu Pro Gln
            180                 185                 190
Ile Gly Glu Glu Asn Trp Gln Glu Thr Glu Ser Phe Tyr Gly Gly Arg
        195                 200                 205
Ala Leu Lys Lys Asp Thr Asn Met Lys Pro Cys Tyr Gly Ser Phe Ala
    210                 215                 220
Arg Pro Thr Asn Glu Lys Gly Gly Gln Ala Lys Leu Lys Val Gly Ala
225                 230                 235                 240
Asp Gly Leu Pro Thr Lys Glu Phe Asp Ile Asp Leu Ala Phe Phe Asp
                245                 250                 255
```

```
Thr Pro Gly Gly Thr Val Thr Gly Gly Thr Glu Glu Tyr Lys Ala Asp
            260                 265                 270
Ile Val Met Tyr Thr Glu Asn Thr Tyr Leu Glu Thr Pro Asp Thr His
        275                 280                 285
Val Val Tyr Lys Pro Gly Lys Asp Asn Thr Ser Ser Lys Ile Asn Leu
    290                 295                 300
Val Gln Gln Ser Met Pro Asn Arg Pro Asn Tyr Ile Gly Phe Arg Asp
305                 310                 315                 320
Asn Phe Ile Gly Leu Met Tyr Tyr Asn Ser Thr Gly Asn Met Gly Val
                325                 330                 335
Leu Ala Gly Gln Ala Ser Gln Leu Asn Ala Val Val Asp Leu Gln Asp
            340                 345                 350
Arg Asn Thr Glu Leu Ser Tyr Gln Leu Leu Leu Asp Ser Leu Gly Asp
        355                 360                 365
Arg Thr Arg Tyr Phe Ser Met Trp Asn Gln Ala Val Asp Ser Tyr Asp
    370                 375                 380
Pro Asp Val Arg Ile Ile Glu Asn His Gly Val Glu Asp Glu Leu Pro
385                 390                 395                 400
Asn Tyr Cys Phe Pro Leu Asp Gly Ser Gly Thr Asn Ala Ala Tyr Gln
                405                 410                 415
Gly Val Lys Val Lys Asn Gly Gln Asp Gly Asp Val Glu Ser Glu Trp
            420                 425                 430
Glu Lys Asp Asp Thr Val Ala Ala Arg Asn Gln Leu Cys Lys Gly Asn
        435                 440                 445
Ile Phe Ala Met Glu Ile Asn Leu Gln Ala Asn Leu Trp Arg Ser Phe
    450                 455                 460
Leu Tyr Ser Asn Val Ala Leu Tyr Leu Pro Asp Ser Tyr Lys Tyr Thr
465                 470                 475                 480
Pro Ala Asn Ile Thr Leu Pro Thr Asn Thr Asn Thr Tyr Asp Tyr Met
                485                 490                 495
Asn Gly Arg Val Val Pro Pro Ser Leu Val Asp Ala Tyr Ile Asn Ile
            500                 505                 510
Gly Ala Arg Trp Ser Leu Asp Pro Met Asp Asn Val Asn Pro Phe Asn
        515                 520                 525
His His Arg Asn Ala Gly Leu Arg Tyr Arg Ser Met Leu Leu Gly Asn
    530                 535                 540
Gly Arg Tyr Val Pro Phe His Ile Gln Val Pro Gln Lys Phe Phe Ala
545                 550                 555                 560
Ile Lys Ser Leu Leu Leu Leu Pro Gly Ser Tyr Thr Tyr Glu Trp Asn
                565                 570                 575
Phe Arg Lys Asp Val Asn Met Ile Leu Gln Ser Ser Leu Gly Asn Asp
            580                 585                 590
Leu Arg Thr Asp Gly Ala Ser Ile Ser Phe Thr Ser Ile Asn Leu Tyr
        595                 600                 605
Ala Thr Phe Phe Pro Met Ala His Asn Thr Ala Ser Thr Leu Glu Ala
    610                 615                 620
Met Leu Arg Asn Asp Thr Asn Asp Gln Ser Phe Asn Asp Tyr Leu Ser
625                 630                 635                 640
Ala Ala Asn Met Leu Tyr Pro Ile Pro Ala Asn Ala Thr Asn Val Pro
                645                 650                 655
Ile Ser Ile Pro Ser Arg Asn Trp Ala Ala Phe Arg Gly Trp Ser Phe
            660                 665                 670
Thr Arg Leu Lys Thr Lys Glu Thr Pro Ser Leu Gly Ser Gly Phe Asp
        675                 680                 685
Pro Tyr Phe Val Tyr Ser Gly Ser Ile Pro Tyr Leu Asp Gly Thr Phe
```

```
    690                 695                 700
Tyr Leu Asn His Thr Phe Lys Lys Val Ser Ile Thr Phe Asp Ser Ser
705                 710                 715                 720
Val Ser Trp Pro Gly Asn Asp Arg Leu Leu Thr Pro Asn Glu Phe Glu
                725                 730                 735
Ile Lys Arg Thr Val Asp Gly Glu Gly Tyr Asn Val Ala Gln Cys Asn
            740                 745                 750
Met Thr Lys Asp Trp Phe Leu Val Gln Met Leu Ala His Tyr Asn Ile
        755                 760                 765
Gly Tyr Gln Gly Phe Tyr Val Pro Glu Gly Tyr Lys Asp Arg Met Tyr
    770                 775                 780
Ser Phe Phe Arg Asn Phe Gln Pro Met Ser Arg Gln Val Val Asp Glu
785                 790                 795                 800
Val Asn Tyr Lys Asp Tyr Gln Ala Val Thr Leu Ala Tyr Gln His Asn
                805                 810                 815
Asn Ser Gly Phe Val Gly Tyr Leu Ala Pro Thr Met Arg Gln Gly Gln
            820                 825                 830
Pro Tyr Pro Ala Asn Tyr Pro Tyr Pro Leu Ile Gly Lys Ser Ala Val
        835                 840                 845
Ala Ser Val Thr Gln Lys Lys Phe Leu Cys Asp Arg Val Met Trp Arg
    850                 855                 860
Ile Pro Phe Ser Ser Asn Phe Met Ser Met Gly Ala Leu Thr Asp Leu
865                 870                 875                 880
Gly Gln Asn Met Leu Tyr Ala Asn Ser Ala His Ala Leu Asp Met Asn
                885                 890                 895
Phe Glu Val Asp Pro Met Asp Glu Ser Thr Leu Leu Tyr Val Val Phe
            900                 905                 910
Glu Val Phe Asp Val Val Arg Val His Gln Pro His Arg Gly Val Ile
        915                 920                 925
Glu Ala Val Tyr Leu Arg Thr Pro Phe Ser Ala Gly Asn Ala Thr Thr
    930                 935                 940
```

<210> 95
<211> 960
<212> PRT
<213> Chimpanzee Adenovirus- ChAd 17 Hexon

<400> 95

```
Met Ala Thr Pro Ser Met Met Pro Gln Trp Ser Tyr Met His Ile Ser
 1                   5                  10                  15
Gly Gln Asp Ala Ser Glu Tyr Leu Ser Pro Gly Leu Val Gln Phe Ala
            20                  25                  30
Arg Ala Thr Glu Ser Tyr Phe Ser Leu Ser Asn Lys Phe Arg Asn Pro
        35                  40                  45
Thr Val Ala Pro Thr His Asp Val Thr Thr Asp Arg Ser Gln Arg Leu
    50                  55                  60
Thr Leu Arg Phe Ile Pro Val Asp Arg Glu Asp Thr Ala Tyr Ser Tyr
65                  70                  75                  80
Lys Ala Arg Phe Thr Leu Ala Val Gly Asp Asn Arg Val Leu Asp Met
                85                  90                  95
Ala Ser Thr Tyr Phe Asp Ile Arg Gly Val Leu Asp Arg Gly Pro Thr
            100                 105                 110
Phe Lys Pro Tyr Ser Gly Thr Ala Tyr Asn Ser Leu Ala Pro Lys Gly
        115                 120                 125
```

```
Ala Pro Asn Ser Cys Glu Trp Glu Gln Glu Glu Thr Gln Ala Val Glu
    130                 135                 140
Glu Ala Ala Glu Glu Glu Glu Glu Asp Ala Asp Gly Gln Ala Glu Glu
145                 150                 155                 160
Glu Gln Ala Ala Thr Lys Lys Thr His Val Tyr Ala Gln Ala Pro Leu
                165                 170                 175
Ser Gly Glu Lys Ile Ser Lys Asp Gly Leu Gln Ile Gly Thr Asp Ala
            180                 185                 190
Thr Ala Thr Glu Gln Lys Pro Ile Tyr Ala Asp Pro Thr Phe Gln Pro
        195                 200                 205
Glu Pro Gln Ile Gly Glu Ser Gln Trp Asn Glu Ala Asp Ala Thr Val
    210                 215                 220
Ala Gly Gly Arg Val Leu Lys Lys Ser Thr Pro Met Lys Pro Cys Tyr
225                 230                 235                 240
Gly Ser Tyr Ala Arg Pro Thr Asn Ala Asn Gly Gly Gln Gly Val Leu
                245                 250                 255
Thr Ala Asn Ala Gln Gly Gln Leu Glu Ser Gln Val Glu Met Gln Phe
            260                 265                 270
Phe Ser Thr Ser Glu Asn Ala Arg Asn Glu Thr Asn Asn Ile Gln Pro
        275                 280                 285
Lys Leu Val Leu Tyr Ser Glu Asp Val His Met Glu Thr Pro Asp Thr
    290                 295                 300
His Leu Ser Tyr Lys Pro Ala Lys Ser Asp Asp Asn Ser Lys Ile Met
305                 310                 315                 320
Leu Gly Gln Gln Ser Met Pro Asn Arg Pro Asn Tyr Ile Gly Phe Arg
                325                 330                 335
Asp Asn Phe Ile Gly Leu Met Tyr Tyr Asn Ser Thr Gly Asn Met Gly
            340                 345                 350
Val Leu Ala Gly Gln Ala Ser Gln Leu Asn Ala Val Val Asp Leu Gln
        355                 360                 365
Asp Arg Asn Thr Glu Leu Ser Tyr Gln Leu Leu Leu Asp Ser Met Gly
    370                 375                 380
Asp Arg Thr Arg Tyr Phe Ser Met Trp Asn Gln Ala Val Asp Ser Tyr
385                 390                 395                 400
Asp Pro Asp Val Arg Ile Ile Glu Asn His Gly Thr Glu Asp Glu Leu
                405                 410                 415
Pro Asn Tyr Cys Phe Pro Leu Gly Gly Ile Gly Val Thr Asp Thr Tyr
            420                 425                 430
Gln Ala Val Lys Thr Asn Asn Gly Asn Asn Gly Gly Gln Val Thr Trp
        435                 440                 445
Thr Lys Asp Glu Thr Phe Ala Asp Arg Asn Glu Ile Gly Val Gly Asn
    450                 455                 460
Asn Phe Ala Met Glu Ile Asn Leu Ser Ala Asn Leu Trp Arg Asn Phe
465                 470                 475                 480
Leu Tyr Ser Asn Val Ala Leu Tyr Leu Pro Asp Lys Leu Lys Tyr Asn
                485                 490                 495
Pro Ser Asn Val Asp Ile Ser Asp Asn Pro Asn Thr Tyr Asp Tyr Met
            500                 505                 510
Asn Lys Arg Val Val Ala Pro Gly Leu Val Asp Cys Tyr Ile Asn Leu
        515                 520                 525
Gly Ala Arg Trp Ser Leu Asp Tyr Met Asp Asn Val Asn Pro Phe Asn
    530                 535                 540
His His Arg Asn Ala Gly Leu Arg Tyr Arg Ser Met Leu Leu Gly Asn
545                 550                 555                 560
Gly Arg Tyr Val Pro Phe His Ile Gln Val Pro Gln Lys Phe Phe Ala
```

```
                565                 570                 575
Ile Lys Asn Leu Leu Leu Leu Pro Gly Ser Tyr Thr Tyr Glu Trp Asn
            580                 585                 590
Phe Arg Lys Asp Val Asn Met Val Leu Gln Ser Ser Leu Gly Asn Asp
        595                 600                 605
Leu Arg Val Asp Gly Ala Ser Ile Lys Phe Glu Ser Ile Cys Leu Tyr
    610                 615                 620
Ala Thr Phe Phe Pro Met Ala His Asn Thr Ala Ser Thr Leu Glu Ala
625                 630                 635                 640
Met Leu Arg Asn Asp Thr Asn Asp Gln Ser Phe Asn Asp Tyr Leu Ser
                645                 650                 655
Ala Ala Asn Met Leu Tyr Pro Ile Pro Ala Asn Ala Thr Asn Val Pro
            660                 665                 670
Ile Ser Ile Pro Ser Arg Asn Trp Ala Ala Phe Arg Gly Trp Ala Phe
        675                 680                 685
Thr Arg Leu Lys Thr Lys Glu Thr Pro Ser Leu Gly Ser Gly Phe Asp
    690                 695                 700
Pro Tyr Tyr Thr Tyr Ser Gly Ser Ile Pro Tyr Leu Asp Gly Thr Phe
705                 710                 715                 720
Tyr Leu Asn His Thr Phe Lys Lys Val Ser Val Thr Phe Asp Ser Ser
                725                 730                 735
Val Ser Trp Pro Gly Asn Asp Arg Leu Leu Thr Pro Asn Glu Phe Glu
            740                 745                 750
Ile Lys Arg Ser Val Asp Gly Glu Gly Tyr Asn Val Ala Gln Cys Asn
        755                 760                 765
Met Thr Lys Asp Trp Phe Leu Val Gln Met Leu Ala Asn Tyr Asn Ile
    770                 775                 780
Gly Tyr Gln Gly Phe Tyr Ile Pro Glu Ser Tyr Lys Asp Arg Met Tyr
785                 790                 795                 800
Ser Phe Phe Arg Asn Phe Gln Pro Met Ser Arg Gln Val Val Asp Gln
                805                 810                 815
Thr Lys Tyr Lys Asp Tyr Gln Glu Val Gly Ile Ile His Gln His Asn
            820                 825                 830
Asn Ser Gly Phe Val Gly Tyr Leu Ala Pro Thr Met Arg Glu Gly Gln
        835                 840                 845
Ala Tyr Pro Ala Asn Phe Pro Tyr Pro Leu Ile Gly Lys Thr Ala Val
    850                 855                 860
Asp Ser Ile Thr Gln Lys Lys Phe Leu Cys Asp Arg Thr Leu Trp Arg
865                 870                 875                 880
Ile Pro Phe Ser Ser Asn Phe Met Ser Met Gly Ala Leu Ser Asp Leu
                885                 890                 895
Gly Gln Asn Leu Leu Tyr Ala Asn Ser Ala His Ala Leu Asp Met Thr
            900                 905                 910
Phe Glu Val Asp Pro Met Asp Glu Pro Thr Leu Leu Tyr Val Leu Phe
        915                 920                 925
Glu Val Phe Asp Val Val Arg Val His Gln Pro His Arg Gly Val Ile
    930                 935                 940
Glu Thr Val Tyr Leu Arg Thr Pro Phe Ser Ala Gly Asn Ala Thr Thr
945                 950                 955                 960
```

<210> 96
<211> 958
<212> PRT
<213> Chimpanzee Adenovirus- ChAd 19 Hexon

<400> 96
Met Ala Thr Pro Ser Met Met Pro Gln Trp Ser Tyr Met His Ile Ser
 1   5   10   15
Gly Gln Asp Ala Ser Glu Tyr Leu Ser Pro Gly Leu Val Gln Phe Ala
            20   25   30
Arg Ala Thr Glu Ser Tyr Phe Ser Leu Ser Asn Lys Phe Arg Asn Pro
        35   40   45
Thr Val Ala Pro Thr His Asp Val Thr Thr Asp Arg Ser Gln Arg Leu
    50   55   60
Thr Leu Arg Phe Ile Pro Val Asp Arg Glu Asp Thr Ala Tyr Ser Tyr
65   70   75   80
Lys Ala Arg Phe Thr Leu Ala Val Gly Asp Asn Arg Val Leu Asp Met
                85   90   95
Ala Ser Thr Tyr Phe Asp Ile Arg Gly Val Leu Asp Arg Gly Pro Thr
            100   105   110
Phe Lys Pro Tyr Ser Gly Thr Ala Tyr Asn Ser Leu Ala Pro Lys Gly
        115   120   125
Ala Pro Asn Ser Cys Glu Trp Glu Gln Leu Glu Glu Ala Gln Ala Ala
    130   135   140
Leu Glu Asp Glu Glu Leu Glu Asp Glu Asp Glu Glu Pro Gln Asp Glu
145   150   155   160
Ala Pro Val Lys Lys Thr His Val Tyr Ala Gln Ala Pro Leu Ser Gly
                165   170   175
Glu Glu Ile Thr Lys Asp Gly Leu Gln Ile Gly Ser Asp Asn Thr Glu
            180   185   190
Ala Gln Ser Lys Pro Ile Tyr Ala Asp Pro Thr Phe Gln Pro Glu Pro
        195   200   205
Gln Ile Gly Glu Ser Gln Trp Asn Glu Ala Asp Ala Thr Val Ala Gly
    210   215   220
Gly Arg Val Leu Lys Lys Thr Thr Pro Met Lys Pro Cys Tyr Gly Ser
225   230   235   240
Tyr Ala Arg Pro Thr Asn Ala Asn Gly Gly Gln Gly Val Leu Val Ala
                245   250   255
Asp Asp Lys Gly Val Leu Gln Ser Lys Val Glu Leu Gln Phe Phe Ser
            260   265   270
Asn Thr Thr Thr Leu Asn Gln Arg Glu Gly Asn Asp Thr Lys Pro Lys
        275   280   285
Val Val Leu Tyr Ser Glu Asp Val His Met Glu Thr Pro Asp Thr His
    290   295   300
Ile Ser Tyr Lys Pro Thr Lys Ser Asp Asp Asn Ser Lys Val Met Leu
305   310   315   320
Gly Gln Gln Ser Met Pro Asn Arg Pro Asn Tyr Ile Gly Phe Arg Asp
                325   330   335
Asn Phe Ile Gly Leu Met Tyr Tyr Asn Ser Thr Gly Asn Met Gly Val
            340   345   350
Leu Ala Gly Gln Ala Ser Gln Leu Asn Ala Val Val Asp Leu Gln Asp
        355   360   365
Arg Asn Thr Glu Leu Ser Tyr Gln Leu Leu Leu Asp Ser Met Gly Asp
    370   375   380
Arg Thr Arg Tyr Phe Ser Met Trp Asn Gln Ala Val Asp Ser Tyr Asp
385   390   395   400
Pro Asp Val Arg Ile Ile Glu Asn His Gly Thr Glu Asp Glu Leu Pro
                405   410   415
Asn Tyr Cys Phe Pro Leu Gly Gly Ile Gly Val Thr Asp Thr Tyr Gln

```
            420                 425                 430
Val Ile Lys Thr Asn Gly Asn Gly Gln Ala Asp Pro Thr Trp Glu Lys
        435                 440                 445
Asp Thr Glu Phe Ala Asp Arg Asn Glu Ile Gly Val Gly Asn Asn Phe
    450                 455                 460
Ala Met Glu Ile Asn Leu Asn Ala Asn Leu Trp Arg Asn Phe Leu Tyr
465                 470                 475                 480
Ser Asn Val Ala Leu Tyr Leu Pro Asp Lys Leu Lys Tyr Asn Pro Ser
                485                 490                 495
Asn Val Asp Ile Ser Asp Asn Pro Asn Thr Tyr Asp Tyr Met Asn Lys
            500                 505                 510
Arg Val Val Ala Pro Gly Leu Val Asp Cys Tyr Ile Asn Leu Gly Ala
        515                 520                 525
Arg Trp Ser Leu Asp Tyr Met Asp Asn Val Asn Pro Phe Asn His His
    530                 535                 540
Arg Asn Ala Gly Leu Arg Tyr Arg Ser Met Leu Leu Gly Asn Gly Arg
545                 550                 555                 560
Tyr Val Pro Phe His Ile Gln Val Pro Gln Lys Phe Phe Ala Ile Lys
                565                 570                 575
Asn Leu Leu Leu Leu Pro Gly Ser Tyr Thr Tyr Glu Trp Asn Phe Arg
            580                 585                 590
Lys Asp Val Asn Met Val Leu Gln Ser Ser Leu Gly Asn Asp Leu Arg
        595                 600                 605
Val Asp Gly Ala Ser Ile Lys Phe Glu Ser Ile Cys Leu Tyr Ala Thr
    610                 615                 620
Phe Phe Pro Met Ala His Asn Thr Ala Ser Thr Leu Glu Ala Met Leu
625                 630                 635                 640
Arg Asn Asp Thr Asn Asp Gln Ser Phe Asn Asp Tyr Leu Ser Ala Ala
                645                 650                 655
Asn Met Leu Tyr Pro Ile Pro Ala Asn Ala Thr Asn Val Pro Ile Ser
            660                 665                 670
Ile Pro Ser Arg Asn Trp Ala Ala Phe Arg Gly Trp Ala Phe Thr Arg
        675                 680                 685
Leu Lys Thr Lys Glu Thr Pro Ser Leu Gly Ser Gly Phe Asp Pro Tyr
    690                 695                 700
Tyr Thr Tyr Ser Gly Ser Ile Pro Tyr Leu Asp Gly Thr Phe Tyr Leu
705                 710                 715                 720
Asn His Thr Phe Lys Lys Val Ser Val Thr Phe Asp Ser Ser Val Ser
                725                 730                 735
Trp Pro Gly Asn Asp Arg Leu Leu Thr Pro Asn Glu Phe Glu Ile Lys
            740                 745                 750
Arg Ser Val Asp Gly Glu Gly Tyr Asn Val Ala Gln Cys Asn Met Thr
        755                 760                 765
Lys Asp Trp Phe Leu Val Gln Met Leu Ala Asn Tyr Asn Ile Gly Tyr
    770                 775                 780
Gln Gly Phe Tyr Ile Pro Glu Ser Tyr Lys Asp Arg Met Tyr Ser Phe
785                 790                 795                 800
Phe Arg Asn Phe Gln Pro Met Ser Arg Gln Val Val Asp Gln Thr Lys
                805                 810                 815
Tyr Lys Asp Tyr Gln Glu Val Gly Ile Ile His Gln His Asn Asn Ser
            820                 825                 830
Gly Phe Val Gly Tyr Leu Ala Pro Thr Met Arg Glu Gly Gln Ala Tyr
        835                 840                 845
Pro Ala Asn Phe Pro Tyr Pro Leu Ile Gly Lys Thr Ala Val Asp Ser
    850                 855                 860
```

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Ile Thr Gln Lys Lys Phe Leu Cys Asp Arg Thr Leu Trp Arg Ile Pro
865                 870                 875                 880
Phe Ser Ser Asn Phe Met Ser Met Gly Ala Leu Thr Asp Leu Gly Gln
                885                 890                 895
Asn Leu Leu Tyr Ala Asn Ser Ala His Ala Leu Asp Met Thr Phe Glu
            900                 905                 910
Val Asp Pro Met Asp Glu Pro Thr Leu Leu Tyr Val Leu Phe Glu Val
        915                 920                 925
Phe Asp Val Val Arg Val His Gln Pro His Arg Gly Val Ile Glu Thr
    930                 935                 940
Val Tyr Leu Arg Thr Pro Phe Ser Ala Gly Asn Ala Thr Thr
945                 950                 955
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<210> 97
<211> 2865
<212> DNA
<213> Chimpanzee Adenovirus- ChAd 8 Hexon

<400> 97

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ctggggaaca agtttaggaa ccccaccgtg gcccccaccc acgatgtgac caccgaccga 180
agccagcggc tgatgctgcg ctttgtgccc gttgatcggg aggacaatac ctactcatac 240
aaagttcgct acacactggc tgtgggcgac aacagagtgc tggatatggc cagcaccttc 300
tttgacatcc ggggggtgct tgacagaggt cccagtttca agccatactc tggcacggct 360
tacaactcct tggctcctaa gggtgccccc aatacatgcc agtggatagc taaagggtcg 420
cccgttcaag atgatgctga acaagctcag gaacaaaaag atgttaccta tacttttggc 480
aatgcgccag taaaagcaga agatgacatt acaaaagacg gattagaagt aggcatacaa 540
attattggtg atgaggagaa tcccatttat gcagataaaa catatcaacc agagccacag 600
gttggtgacg agcaatggca tgacacaact ggaaccactg agcagtatgg aggcagagct 660
cttaagccag ctacaaacat gaggccatgc tatggctctt ttgccagacc tacaaacaaa 720
aaaggagggc aagctaaaac cagaaaagta gaaaaaactg aaggtgacaa aaagactgaa 780
gttgaagaac ttgacattga tatggatttt tatgatgcaa gatctaaaaa acaaggctat 840
gatcctcaaa tagtgctata ttcagaaaat gtaaatctgg aaacgcccga cactcatatt 900
gtgtacaaac cgggaactga tgaaaccagt tcctccacta atttgggcca gcaagctatg 960
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ttgcaggaca ggaacacaga actgtcctac cagctgctgc ttgactctct gggtgacaga 1140
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attgaaaatc atggtgtgga agatgaactt cccaattatt gtttcccatt ggatggtgtt 1260
ggtccaatta cagaaaccta tcaaggtatc aagccaaaaa cagcagacaa tgcaaatgac 1320
caatgggaaa aaaataccga agtaaatgga gctaatgaaa taggaaaggg aaacaattat 1380
gcaatggaaa ttaatctaca agctaacctc tggagaagtt ttctttactc caacgtggct 1440
ctgtatcttc cagacggtta caaatatacc ccagccaatg ttacgctgcc agacaacaaa 1500
aatacctatg ggtacataaa cggacgagta gtgtctccat ctttggtgga ttcatacatc 1560
aacattggag ccagatggtc tttggatctt atggacaatg tcaacccatt taatcaccac 1620
cgcaatgctg ggctgcgcta ccgttccatg cttcttggca atggacgcta tgtgcccttc 1680
cacatccaag tgccgcagaa attctttgct atcaagaact tgctgcttct gccaggctcc 1740
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aatgatctca gaactgatgg agccagcatc agttttacca gcatcaacct ctatgccacc 1860
tttttcccaa tggctcacaa cactgcttcc acccttgaag ccatgctgcg caatgacacc 1920
aatgaccagt cattcaacga ctacctctct gcagccaaca tgctctaccc catccctgcc 1980
aatgccacta acattcccat ctccattccc tctcgcaact gggctgcctt caggggctgg 2040
tccttcacca gactcaaaac caaggagact ccctctttgg gatcagggtt cgatccctac 2100
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```
tttgtctatt caggctccat tccctacctg gatggtacct tctacctcaa ccacactttc 2160
aagaaggtct ccatcatgtt tgactcctca gtcagctggc cgggcaatga cagactgttg 2220
tgtcccaatg agtttgaaat caagcgcact gtggatgggg aagggtacaa cgtggctcaa 2280
tgcaacatga ccaaggattg gttcttggtc cagatgcttg ccaactacaa cattggctac 2340
cagggcttct acatcccaga ggggtacaag gatcgcatgt actccttctt cagaaacttc 2400
cagcccatga gcagacaggt agttgatgaa gtcaattaca aggagtacca agctgtcaca 2460
cttgcttacc agcacaacaa ctctggtttt gtgggttacc atgcacccac tcttcgtcag 2520
ggccaaccat acccagctaa ctacccctac ccgctcattg gaaccactgc tgtcaccagc 2580
gtcacccaga aaaagttctt gtgcgacagg accatgtggc gcatcccatt ctccagcaac 2640
ttcatgtcca tgggtgccct taccgacctg gggcagaaca tgctttatgc caactcagcc 2700
catgcgctgg acatgacttt tgaggtggat cccatggatg agcccacact gctttatctt 2760
ctttttgaag tcttcgacgt ggtcagagtg caccagccac accgcggcgt catcgaggct 2820
gtctacctgc gtaccccatt ctcagctggt aacgccacca cataa                  2865

<210> 98
<211> 954
<212> PRT
<213> Chimpanzee Adenovirus ChAd 8

<400> 98
Met Ala Thr Pro Ser Met Leu Pro Gln Trp Ala Tyr Met His Ile Ala
 1               5                  10                  15
Gly Gln Asp Ala Ser Glu Tyr Leu Ser Pro Gly Leu Val Gln Phe Ala
            20                  25                  30
Arg Ala Thr Asp Thr Tyr Phe Asn Leu Gly Asn Lys Phe Arg Asn Pro
        35                  40                  45
Thr Val Ala Pro Thr His Asp Val Thr Thr Asp Arg Ser Gln Arg Leu
    50                  55                  60
Met Leu Arg Phe Val Pro Val Asp Arg Glu Asp Asn Thr Tyr Ser Tyr
65                  70                  75                  80
Lys Val Arg Tyr Thr Leu Ala Val Gly Asp Asn Arg Val Leu Asp Met
                85                  90                  95
Ala Ser Thr Phe Phe Asp Ile Arg Gly Val Leu Asp Arg Gly Pro Ser
            100                 105                 110
Phe Lys Pro Tyr Ser Gly Thr Ala Tyr Asn Ser Leu Ala Pro Lys Gly
        115                 120                 125
Ala Pro Asn Thr Cys Gln Trp Ile Ala Lys Gly Ser Pro Val Gln Asp
    130                 135                 140
Asp Ala Glu Gln Ala Gln Glu Gln Lys Asp Val Thr Tyr Thr Phe Gly
145                 150                 155                 160
Asn Ala Pro Val Lys Ala Glu Asp Asp Ile Thr Lys Asp Gly Leu Glu
                165                 170                 175
Val Gly Ile Gln Ile Ile Gly Asp Glu Glu Asn Pro Ile Tyr Ala Asp
            180                 185                 190
Lys Thr Tyr Gln Pro Glu Pro Gln Val Gly Asp Glu Gln Trp His Asp
        195                 200                 205
Thr Thr Gly Thr Thr Glu Gln Tyr Gly Gly Arg Ala Leu Lys Pro Ala
    210                 215                 220
Thr Asn Met Arg Pro Cys Tyr Gly Ser Phe Ala Arg Pro Thr Asn Lys
225                 230                 235                 240
Lys Gly Gly Gln Ala Lys Thr Arg Lys Val Glu Lys Thr Glu Gly Asp
                245                 250                 255
Lys Lys Thr Glu Val Glu Glu Leu Asp Ile Asp Met Asp Phe Tyr Asp
            260                 265                 270
Ala Arg Ser Lys Lys Gln Gly Tyr Asp Pro Gln Ile Val Leu Tyr Ser
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        275                 280                 285
Glu Asn Val Asn Leu Glu Thr Pro Asp Thr His Ile Val Tyr Lys Pro
    290                 295                 300
Gly Thr Asp Glu Thr Ser Ser Ser Thr Asn Leu Gly Gln Gln Ala Met
305                 310                 315                 320
Pro Asn Arg Pro Asn Tyr Ile Gly Phe Arg Asp Asn Phe Ile Gly Leu
                325                 330                 335
Met Tyr Tyr Asn Ser Thr Gly Asn Met Gly Val Leu Ala Gly Gln Ala
            340                 345                 350
Ser Gln Leu Asn Ala Val Val Asp Leu Gln Asp Arg Asn Thr Glu Leu
        355                 360                 365
Ser Tyr Gln Leu Leu Leu Asp Ser Leu Gly Asp Arg Thr Arg Tyr Phe
    370                 375                 380
Ser Met Trp Asn Gln Ala Val Asp Ser Tyr Asp Pro Asp Val Arg Ile
385                 390                 395                 400
Ile Glu Asn His Gly Val Glu Asp Glu Leu Pro Asn Tyr Cys Phe Pro
                405                 410                 415
Leu Asp Gly Val Gly Pro Ile Thr Glu Thr Tyr Gln Gly Ile Lys Pro
            420                 425                 430
Lys Thr Ala Asp Asn Ala Asn Asp Gln Trp Glu Lys Asn Thr Glu Val
        435                 440                 445
Asn Gly Ala Asn Glu Ile Gly Lys Gly Asn Asn Tyr Ala Met Glu Ile
    450                 455                 460
Asn Leu Gln Ala Asn Leu Trp Arg Ser Phe Leu Tyr Ser Asn Val Ala
465                 470                 475                 480
Leu Tyr Leu Pro Asp Gly Tyr Lys Tyr Thr Pro Ala Asn Val Thr Leu
                485                 490                 495
Pro Asp Asn Lys Asn Thr Tyr Gly Tyr Ile Asn Gly Arg Val Val Ser
            500                 505                 510
Pro Ser Leu Val Asp Ser Tyr Ile Asn Ile Gly Ala Arg Trp Ser Leu
        515                 520                 525
Asp Leu Met Asp Asn Val Asn Pro Phe Asn His His Arg Asn Ala Gly
    530                 535                 540
Leu Arg Tyr Arg Ser Met Leu Leu Gly Asn Gly Arg Tyr Val Pro Phe
545                 550                 555                 560
His Ile Gln Val Pro Gln Lys Phe Phe Ala Ile Lys Asn Leu Leu Leu
                565                 570                 575
Leu Pro Gly Ser Tyr Thr Tyr Glu Trp Asn Phe Arg Lys Asp Val Asn
            580                 585                 590
Met Val Leu Gln Ser Ser Leu Gly Asn Asp Leu Arg Thr Asp Gly Ala
        595                 600                 605
Ser Ile Ser Phe Thr Ser Ile Asn Leu Tyr Ala Thr Phe Phe Pro Met
    610                 615                 620
Ala His Asn Thr Ala Ser Thr Leu Glu Ala Met Leu Arg Asn Asp Thr
625                 630                 635                 640
Asn Asp Gln Ser Phe Asn Asp Tyr Leu Ser Ala Ala Asn Met Leu Tyr
                645                 650                 655
Pro Ile Pro Ala Asn Ala Thr Asn Ile Pro Ile Ser Ile Pro Ser Arg
            660                 665                 670
Asn Trp Ala Ala Phe Arg Gly Trp Ser Phe Thr Arg Leu Lys Thr Lys
        675                 680                 685
Glu Thr Pro Ser Leu Gly Ser Gly Phe Asp Pro Tyr Phe Val Tyr Ser
    690                 695                 700
Gly Ser Ile Pro Tyr Leu Asp Gly Thr Phe Tyr Leu Asn His Thr Phe
705                 710                 715                 720
```

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Lys Lys Val Ser Ile Met Phe Asp Ser Ser Val Ser Trp Pro Gly Asn
                725                 730                 735
Asp Arg Leu Leu Cys Pro Asn Glu Phe Glu Ile Lys Arg Thr Val Asp
            740                 745                 750
Gly Glu Gly Tyr Asn Val Ala Gln Cys Asn Met Thr Lys Asp Trp Phe
        755                 760                 765
Leu Val Gln Met Leu Ala Asn Tyr Asn Ile Gly Tyr Gln Gly Phe Tyr
    770                 775                 780
Ile Pro Glu Gly Tyr Lys Asp Arg Met Tyr Ser Phe Phe Arg Asn Phe
785                 790                 795                 800
Gln Pro Met Ser Arg Gln Val Val Asp Glu Val Asn Tyr Lys Glu Tyr
                805                 810                 815
Gln Ala Val Thr Leu Ala Tyr Gln His Asn Asn Ser Gly Phe Val Gly
            820                 825                 830
Tyr His Ala Pro Thr Leu Arg Gln Gly Gln Pro Tyr Pro Ala Asn Tyr
        835                 840                 845
Pro Tyr Pro Leu Ile Gly Thr Thr Ala Val Thr Ser Val Thr Gln Lys
    850                 855                 860
Lys Phe Leu Cys Asp Arg Thr Met Trp Arg Ile Pro Phe Ser Ser Asn
865                 870                 875                 880
Phe Met Ser Met Gly Ala Leu Thr Asp Leu Gly Gln Asn Met Leu Tyr
                885                 890                 895
Ala Asn Ser Ala His Ala Leu Asp Met Thr Phe Glu Val Asp Pro Met
            900                 905                 910
Asp Glu Pro Thr Leu Leu Tyr Leu Leu Phe Glu Val Phe Asp Val Val
        915                 920                 925
Arg Val His Gln Pro His Arg Gly Val Ile Glu Ala Val Tyr Leu Arg
    930                 935                 940
Thr Pro Phe Ser Ala Gly Asn Ala Thr Thr
945                 950
```

<210> 99
<211> 2871
<212> DNA
<213> Chimpanzee Adenovirus- ChAd 22 Hexon

<400> 99

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ctggggaaca agtttaggaa ccctaccgtg gcgcccaccc atgatgtgac caccgaccgc 180
agtcaacggc tgatgctccg ctttgtgccc gttgaccggg aggacaatac ctactcatac 240
aaagttcgat acaccttggc tgtgggcgac aacagagtgc tggatatggc cagtactttc 300
tttgacattc ggggtgtgtt ggatagaggc cctagcttca agccatattc tggcactgct 360
tacaactcat tggcccctaa gggcgctccc aatacatctc agtggattgc tgaaggcgta 420
aaaaaagaaa atggggaagc tgacaatgaa gcagctgtcg aagaggaaga ggaagagaaa 480
aatcttacca cttacacttt tggaaatgcc ccagtgaaag cagaaggtgg tgatatcact 540
aaagacaaag gtcttccaat tggttcagaa attacagacg gcgaagccaa accaatttat 600
gcagataaac tataccaacc agaacctcag gtgggagagg aaacttggac tgacacagat 660
ggaacaactg agaagtatgg tggtagagct ctaaagccag aaactaaaat gaaaccctgc 720
tatgggtctt ttgctaaacc cactaacgtc aaaggcggac aggcaaaaca aaaaactact 780
gaacaactgc aaaaccagca ggttgaatat gatattgaca tgaacttttt tgatcaagcg 840
tcacagaaag caaacttcag tccaaaaatt gtgatgtatg cagaaaatgt agacttggaa 900
accccagaca ctcacgtggt gtacaaacct ggtacttcag aagaaagttc tcatgctaat 960
ctcggtcaac aatctatgcc caacagaccc aactacattg gctttagaga taactttatt 1020
```

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ggacttatgt actacaacag tactggcaac atgggagtgc tggcaggtca agcatcccaa 1080
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gattctctgg gtgacagaac cagatacttc agcatgtgga atcaagcagt cgatagctat 1200
gatcctgatg tgcgcattat tgaaaatcat ggggtggaag atgagcttcc caactactgc 1260
tttccattgg atggagtagg ggtaccaaca actagttaca aaataattga accaaatgga 1320
gagggtgcag attggaaaga gcctgacata aatggaacaa gtgaaattgg acaaggaaat 1380
ctctttgcca tggaaattaa cctccaagct aatctctgga gaagttttct ttattccaat 1440
gtggctctgt atctcccaga ctcctacaaa tacaccccag ccaatgtcac tcttccaact 1500
aacaccaaca cttatgacta catgaatggg cgggtggttc ccccatccct agtggatacc 1560
tacgtaaaca ttggcgccag atggtctttg gatgccatgg acaatgtcaa ccccttaac 1620
catcaccgca acgctggcct gcgataccgg tccatgcttt tgggcaatgg tcgctacgtg 1680
cctttccaca ttcaagtgcc tcagaaattc tttgctgtga agaacctgct gcttctaccc 1740
ggttcttaca cctacgagtg gaacttcaga aaggatgtga acatggtcct gcagagttcc 1800
cttggtaatg atctccgggt cgatggtgcc agcatcagtt ttaccagcat caatctctat 1860
gccaccttct tccccatggc ccacaacact gcctccaccc ttgaagccat gctgcgcaat 1920
gacaccaatg atcaatcatt caatgactac ctttctgcag ccaacatgct ctaccccatc 1980
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ccctactttg tttactctgg ttctatacct tacctggatg gtaccttcta ccttaaccac 2160
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ttgctaactc caaatgagtt cgaaatcaag cgcacagttg atggggaagg ctacaatgtg 2280
gcccaatgta acatgaccaa agactggttc ctggtccaga tgcttgccaa ctacaacatt 2340
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gtcgccgtac cctaccagca taataactct ggctttgtgg gttacatggc tcctaccatg 2520
cgtcagggtc aagcgtaccc tgctaactac ccataccccc taattggaac cactgcagta 2580
accagtgtca cccagaaaaa attcctgtgc gacaggacca tgtggcgcat cccattctct 2640
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tcagcccatg cgctggacat gacttttgag gtggatccca tggatgagcc caccctgctt 2760
tatcttcttt ttgaagtatt cgacgtggtc agagtgcacc aaccacaccg cggcgtcatc 2820
gaggccgtct acctgcgcac accgttctcg gctggtaacg ccaccacata a          2871
```

<210> 100
<211> 956
<212> PRT
<213> Chimpanzee Adenovirus- ChAd 22 Hexon

<400> 100

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Gly Gln Asp Ala Ser Glu Tyr Leu Ser Pro Gly Leu Val Gln Phe Ala
            20                  25                  30
Arg Ala Thr Asp Thr Tyr Phe Asn Leu Gly Asn Lys Phe Arg Asn Pro
        35                  40                  45
Thr Val Ala Pro Thr His Asp Val Thr Thr Asp Arg Ser Gln Arg Leu
    50                  55                  60
Met Leu Arg Phe Val Pro Val Asp Arg Glu Asp Asn Thr Tyr Ser Tyr
65                  70                  75                  80
Lys Val Arg Tyr Thr Leu Ala Val Gly Asp Asn Arg Val Leu Asp Met
                85                  90                  95
Ala Ser Thr Phe Phe Asp Ile Arg Gly Val Leu Asp Arg Gly Pro Ser
            100                 105                 110
Phe Lys Pro Tyr Ser Gly Thr Ala Tyr Asn Ser Leu Ala Pro Lys Gly
        115                 120                 125
Ala Pro Asn Thr Ser Gln Trp Ile Ala Glu Gly Val Lys Lys Glu Asn
```

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    130                 135                 140
Gly Glu Ala Asp Asn Glu Ala Ala Val Glu Glu Glu Glu Glu Glu Lys
145                 150                 155                 160
Asn Leu Thr Thr Tyr Thr Phe Gly Asn Ala Pro Val Lys Ala Glu Gly
                165                 170                 175
Gly Asp Ile Thr Lys Asp Lys Gly Leu Pro Ile Gly Ser Glu Ile Thr
            180                 185                 190
Asp Gly Glu Ala Lys Pro Ile Tyr Ala Asp Lys Leu Tyr Gln Pro Glu
        195                 200                 205
Pro Gln Val Gly Glu Glu Thr Trp Thr Asp Thr Asp Gly Thr Thr Glu
    210                 215                 220
Lys Tyr Gly Gly Arg Ala Leu Lys Pro Glu Thr Lys Met Lys Pro Cys
225                 230                 235                 240
Tyr Gly Ser Phe Ala Lys Pro Thr Asn Val Lys Gly Gly Gln Ala Lys
                245                 250                 255
Gln Lys Thr Thr Glu Gln Leu Gln Asn Gln Gln Val Glu Tyr Asp Ile
            260                 265                 270
Asp Met Asn Phe Phe Asp Gln Ala Ser Gln Lys Ala Asn Phe Ser Pro
        275                 280                 285
Lys Ile Val Met Tyr Ala Glu Asn Val Asp Leu Glu Thr Pro Asp Thr
    290                 295                 300
His Val Val Tyr Lys Pro Gly Thr Ser Glu Glu Ser Ser His Ala Asn
305                 310                 315                 320
Leu Gly Gln Gln Ser Met Pro Asn Arg Pro Asn Tyr Ile Gly Phe Arg
                325                 330                 335
Asp Asn Phe Ile Gly Leu Met Tyr Tyr Asn Ser Thr Gly Asn Met Gly
            340                 345                 350
Val Leu Ala Gly Gln Ala Ser Gln Leu Asn Ala Val Val Asp Leu Gln
        355                 360                 365
Asp Arg Asn Thr Glu Leu Ser Tyr Gln Leu Leu Leu Asp Ser Leu Gly
    370                 375                 380
Asp Arg Thr Arg Tyr Phe Ser Met Trp Asn Gln Ala Val Asp Ser Tyr
385                 390                 395                 400
Asp Pro Asp Val Arg Ile Ile Glu Asn His Gly Val Glu Asp Glu Leu
                405                 410                 415
Pro Asn Tyr Cys Phe Pro Leu Asp Gly Val Gly Val Pro Thr Thr Ser
            420                 425                 430
Tyr Lys Ile Ile Glu Pro Asn Gly Glu Gly Ala Asp Trp Lys Glu Pro
        435                 440                 445
Asp Ile Asn Gly Thr Ser Glu Ile Gly Gln Gly Asn Leu Phe Ala Met
    450                 455                 460
Glu Ile Asn Leu Gln Ala Asn Leu Trp Arg Ser Phe Leu Tyr Ser Asn
465                 470                 475                 480
Val Ala Leu Tyr Leu Pro Asp Ser Tyr Lys Tyr Thr Pro Ala Asn Val
                485                 490                 495
Thr Leu Pro Thr Asn Thr Asn Thr Tyr Asp Tyr Met Asn Gly Arg Val
            500                 505                 510
Val Pro Pro Ser Leu Val Asp Thr Tyr Val Asn Ile Gly Ala Arg Trp
        515                 520                 525
Ser Leu Asp Ala Met Asp Asn Val Asn Pro Phe Asn His His Arg Asn
    530                 535                 540
Ala Gly Leu Arg Tyr Arg Ser Met Leu Leu Gly Asn Gly Arg Tyr Val
545                 550                 555                 560
Pro Phe His Ile Gln Val Pro Gln Lys Phe Phe Ala Val Lys Asn Leu
                565                 570                 575
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Leu Leu Leu Pro Gly Ser Tyr Thr Tyr Glu Trp Asn Phe Arg Lys Asp
            580                 585                 590
Val Asn Met Val Leu Gln Ser Ser Leu Gly Asn Asp Leu Arg Val Asp
        595                 600                 605
Gly Ala Ser Ile Ser Phe Thr Ser Ile Asn Leu Tyr Ala Thr Phe Phe
    610                 615                 620
Pro Met Ala His Asn Thr Ala Ser Thr Leu Glu Ala Met Leu Arg Asn
625                 630                 635                 640
Asp Thr Asn Asp Gln Ser Phe Asn Asp Tyr Leu Ser Ala Ala Asn Met
                645                 650                 655
Leu Tyr Pro Ile Pro Ala Asn Ala Thr Asn Val Pro Ile Ser Ile Pro
            660                 665                 670
Ser Arg Asn Trp Ala Ala Phe Arg Gly Trp Ser Phe Thr Arg Leu Lys
        675                 680                 685
Thr Lys Glu Thr Pro Ser Leu Gly Ser Gly Phe Asp Pro Tyr Phe Val
    690                 695                 700
Tyr Ser Gly Ser Ile Pro Tyr Leu Asp Gly Thr Phe Tyr Leu Asn His
705                 710                 715                 720
Thr Phe Lys Lys Val Ser Ile Met Phe Asp Ser Ser Val Ser Trp Pro
                725                 730                 735
Gly Asn Asp Arg Leu Leu Thr Pro Asn Glu Phe Glu Ile Lys Arg Thr
            740                 745                 750
Val Asp Gly Glu Gly Tyr Asn Val Ala Gln Cys Asn Met Thr Lys Asp
        755                 760                 765
Trp Phe Leu Val Gln Met Leu Ala Asn Tyr Asn Ile Gly Tyr Gln Gly
    770                 775                 780
Phe Tyr Val Pro Glu Gly Tyr Lys Asp Arg Met Tyr Ser Phe Phe Arg
785                 790                 795                 800
Asn Phe Gln Pro Met Ser Arg Gln Val Val Asp Glu Ile Asn Tyr Lys
                805                 810                 815
Asp Tyr Lys Ala Val Ala Val Pro Tyr Gln His Asn Asn Ser Gly Phe
            820                 825                 830
Val Gly Tyr Met Ala Pro Thr Met Arg Gln Gly Gln Ala Tyr Pro Ala
        835                 840                 845
Asn Tyr Pro Tyr Pro Leu Ile Gly Thr Thr Ala Val Thr Ser Val Thr
    850                 855                 860
Gln Lys Lys Phe Leu Cys Asp Arg Thr Met Trp Arg Ile Pro Phe Ser
865                 870                 875                 880
Ser Asn Phe Met Ser Met Gly Ala Leu Thr Asp Leu Gly Gln Asn Leu
                885                 890                 895
Leu Tyr Ala Asn Ser Ala His Ala Leu Asp Met Thr Phe Glu Val Asp
            900                 905                 910
Pro Met Asp Glu Pro Thr Leu Leu Tyr Leu Leu Phe Glu Val Phe Asp
        915                 920                 925
Val Val Arg Val His Gln Pro His Arg Gly Val Ile Glu Ala Val Tyr
    930                 935                 940
Leu Arg Thr Pro Phe Ser Ala Gly Asn Ala Thr Thr
945                 950                 955
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<210> 101
<211> 2865
<212> DNA
<213> Chimpanzee Adenovirus- ChAd 24 Hexon

<400> 101
atggcgaccc catcgatgat gccgcagtgg tcgtacatgc acatctcggg ccaggacgcc 60
tcggagtacc tgagccccgg gctggtgcag ttcgcccgcg ccaccgagag ctacttcagc 120
ctgagtaaca agtttaggaa ccccacggtg gcgcccacgc acgatgtgac caccgaccgg 180
tcccagcgcc tgacgctgcg gttcatcccc gtggaccgcg aggacaccgc gtactcgtac 240
aaggcgcggt tcaccctggc cgtgggcgac aaccgcgtgc tggacatggc ctccacctac 300
tttgacatcc gcggcgtgct ggaccgcggc cccaccttca agccctactc cggcaccgcc 360
tacaactccc tggcccccaa gggcgcgccc aacccatgcg agtgggatga ggctgctact 420
gcccttgaca ttgatttgaa cgcagaagaa gatgaagaag gcgatgaagc ccaaggggaa 480
gcagatcagc agaaaactca tgtatttggc caggcgccat actccggaca gaacattaca 540
aaagaaggca tacagatagg cattgatgct accagtcaag cccaaacacc tctatatgcc 600
gacaaaacat tccaacccga acctcaggtt ggagaatcac aatggaatga gacagagatt 660
agccatggag cgggacgggt gctaaaaaag accactctca tgaaaccttg ctatgggtca 720
tatgcaaggc ctactaatga gaacggaggt cagggcatcc tcctggaaca agatggaaag 780
aaagaaagtc aagtggaaat gcaatttttc tccactactc aggcagctgc gggtaattca 840
gataatccta ctccaaagct tgttttgtac agcgaggatg ttaacctgga aacaccagat 900
acacacattt catacatgcc cactaacaac gaaaccaatt caagagaact gttgggacaa 960
caggccatgc ccaacaggcc taattacatc ggcttcagag acaactttat cggtctcatg 1020
tactacaaca gcactggcaa catgggagtg cttgcaggtc aggcctctca gttgaatgca 1080
gtggtggact tgcaagacag aaacacagaa ctgtcctacc agctcttgct tgattccatg 1140
ggtgacagaa ccagatattt ctccatgtgg aatcaggcag tggacagtta tgacccagat 1200
gtcagaatta ttgaaaatca tggaaccgaa gacgagctcc ccaactactg ttttcctctg 1260
ggtggcataa tcaatacgga aacttttaca aaagtcaagc ctaaagctgg acaggacgct 1320
cagtgggaaa aagattcaga attttcagat aaaaatgaaa taagagtggg aaacaacttc 1380
gctatggaaa tcaacatcaa tgccaacctg tggaggaact tcctgtactc caacgtggcc 1440
ctgtacctgc cagacaagct taagtatact ccatccaatg tgcaaatttc caacaacccc 1500
aactcctacg attacatgaa caagcgagtg gtggccccgg ggctggtgga ctgctacatc 1560
aacctgggcg cgcggtggtc gctggactac atggacaacg tcaacccctt caaccaccac 1620
cgcaacgcgg gcctgcgcta ccgctccatg ctcctgggca acgggcgcta cgtgcccttc 1680
cacatccagg tgccccagaa gttctttgcc atcaagaacc tcctcctcct gccgggctcc 1740
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aacgatctca gggtggacgg ggccagcatc aagttcgaga gcatctgcct ctacgccacc 1860
ttcttcccca tggcccacaa cacggcctcc acgctcgagg ccatgctcag gaacgacacc 1920
aacgaccagt ccttcaatga ctacctctcc gccgccaaca tgctctaccc catccccgcc 1980
aacgccacca acgtccccat ctccatcccc tcgcgcaact gggcggcctt ccgcggctgg 2040
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tacacctact cgggatccat tccctacctg gacggcacct tctacctcaa ccacactttc 2160
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tgcaacatga ccaaggactg gttcctggtc cagatgctgg ccaactacaa catcggctac 2340
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cagcccatga gccggcaggt ggtggaccag accaagtaca aggactacca ggaggtgggc 2460
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ggacaggcct accccgccaa cttcccctac ccgctcatag gcaagaccgc ggtcgacagc 2580
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ttcatgtcca tgggtgcgct cacggacctg ggccagaacc tgctctatgc caactccgcc 2700
cacgcgctcg acatgacctt cgaggtcgac cccatggacg agcccaccct tctctatgtt 2760
ctgttcgaag tctttgacgt ggtccgggtc caccagccgc accgcggcgt catcgagacc 2820
gtgtacctgc gcacgccctt ctcggccggc aacgccacca cctaa 2865

<210> 102
<211> 954
<212> PRT
<213> Chimpanzee Adenovirus- ChAd 24 Hexon

<400> 102

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Gly Gln Asp Ala Ser Glu Tyr Leu Ser Pro Gly Leu Val Gln Phe Ala
            20                  25                  30
Arg Ala Thr Glu Ser Tyr Phe Ser Leu Ser Asn Lys Phe Arg Asn Pro
        35                  40                  45
Thr Val Ala Pro Thr His Asp Val Thr Thr Asp Arg Ser Gln Arg Leu
    50                  55                  60
Thr Leu Arg Phe Ile Pro Val Asp Arg Glu Asp Thr Ala Tyr Ser Tyr
65                  70                  75                  80
Lys Ala Arg Phe Thr Leu Ala Val Gly Asp Asn Arg Val Leu Asp Met
                85                  90                  95
Ala Ser Thr Tyr Phe Asp Ile Arg Gly Val Leu Asp Arg Gly Pro Thr
            100                 105                 110
Phe Lys Pro Tyr Ser Gly Thr Ala Tyr Asn Ser Leu Ala Pro Lys Gly
        115                 120                 125
Ala Pro Asn Pro Cys Glu Trp Asp Glu Ala Ala Thr Ala Leu Asp Ile
    130                 135                 140
Asp Leu Asn Ala Glu Glu Asp Glu Glu Gly Asp Glu Ala Gln Gly Glu
145                 150                 155                 160
Ala Asp Gln Gln Lys Thr His Val Phe Gly Gln Ala Pro Tyr Ser Gly
                165                 170                 175
Gln Asn Ile Thr Lys Glu Gly Ile Gln Ile Gly Ile Asp Ala Thr Ser
            180                 185                 190
Gln Ala Gln Thr Pro Leu Tyr Ala Asp Lys Thr Phe Gln Pro Glu Pro
        195                 200                 205
Gln Val Gly Glu Ser Gln Trp Asn Glu Thr Glu Ile Ser His Gly Ala
    210                 215                 220
Gly Arg Val Leu Lys Lys Thr Thr Leu Met Lys Pro Cys Tyr Gly Ser
225                 230                 235                 240
Tyr Ala Arg Pro Thr Asn Glu Asn Gly Gly Gln Gly Ile Leu Leu Glu
                245                 250                 255
Gln Asp Gly Lys Lys Glu Ser Gln Val Glu Met Gln Phe Phe Ser Thr
            260                 265                 270
Thr Gln Ala Ala Ala Gly Asn Ser Asp Asn Pro Thr Pro Lys Leu Val
        275                 280                 285
Leu Tyr Ser Glu Asp Val Asn Leu Glu Thr Pro Asp Thr His Ile Ser
    290                 295                 300
Tyr Met Pro Thr Asn Asn Glu Thr Asn Ser Arg Glu Leu Leu Gly Gln
305                 310                 315                 320
Gln Ala Met Pro Asn Arg Pro Asn Tyr Ile Gly Phe Arg Asp Asn Phe
                325                 330                 335
Ile Gly Leu Met Tyr Tyr Asn Ser Thr Gly Asn Met Gly Val Leu Ala
            340                 345                 350
Gly Gln Ala Ser Gln Leu Asn Ala Val Val Asp Leu Gln Asp Arg Asn
        355                 360                 365
Thr Glu Leu Ser Tyr Gln Leu Leu Leu Asp Ser Met Gly Asp Arg Thr
    370                 375                 380
Arg Tyr Phe Ser Met Trp Asn Gln Ala Val Asp Ser Tyr Asp Pro Asp
385                 390                 395                 400
Val Arg Ile Ile Glu Asn His Gly Thr Glu Asp Glu Leu Pro Asn Tyr
                405                 410                 415
Cys Phe Pro Leu Gly Gly Ile Ile Asn Thr Glu Thr Phe Thr Lys Val
            420                 425                 430
```

```
Lys Pro Lys Ala Gly Gln Asp Ala Gln Trp Glu Lys Asp Ser Glu Phe
        435                 440                 445
Ser Asp Lys Asn Glu Ile Arg Val Gly Asn Asn Phe Ala Met Glu Ile
    450                 455                 460
Asn Ile Asn Ala Asn Leu Trp Arg Asn Phe Leu Tyr Ser Asn Val Ala
465                 470                 475                 480
Leu Tyr Leu Pro Asp Lys Leu Lys Tyr Thr Pro Ser Asn Val Gln Ile
                485                 490                 495
Ser Asn Asn Pro Asn Ser Tyr Asp Tyr Met Asn Lys Arg Val Val Ala
            500                 505                 510
Pro Gly Leu Val Asp Cys Tyr Ile Asn Leu Gly Ala Arg Trp Ser Leu
        515                 520                 525
Asp Tyr Met Asp Asn Val Asn Pro Phe Asn His His Arg Asn Ala Gly
    530                 535                 540
Leu Arg Tyr Arg Ser Met Leu Leu Gly Asn Gly Arg Tyr Val Pro Phe
545                 550                 555                 560
His Ile Gln Val Pro Gln Lys Phe Phe Ala Ile Lys Asn Leu Leu Leu
                565                 570                 575
Leu Pro Gly Ser Tyr Thr Tyr Glu Trp Asn Phe Arg Lys Asp Val Asn
            580                 585                 590
Met Val Leu Gln Ser Ser Leu Gly Asn Asp Leu Arg Val Asp Gly Ala
        595                 600                 605
Ser Ile Lys Phe Glu Ser Ile Cys Leu Tyr Ala Thr Phe Phe Pro Met
    610                 615                 620
Ala His Asn Thr Ala Ser Thr Leu Glu Ala Met Leu Arg Asn Asp Thr
625                 630                 635                 640
Asn Asp Gln Ser Phe Asn Asp Tyr Leu Ser Ala Ala Asn Met Leu Tyr
                645                 650                 655
Pro Ile Pro Ala Asn Ala Thr Asn Val Pro Ile Ser Ile Pro Ser Arg
            660                 665                 670
Asn Trp Ala Ala Phe Arg Gly Trp Ala Phe Thr Arg Leu Lys Thr Lys
        675                 680                 685
Glu Thr Pro Ser Leu Gly Ser Gly Phe Asp Pro Tyr Tyr Thr Tyr Ser
    690                 695                 700
Gly Ser Ile Pro Tyr Leu Asp Gly Thr Phe Tyr Leu Asn His Thr Phe
705                 710                 715                 720
Lys Lys Val Ser Val Thr Phe Asp Ser Ser Val Ser Trp Pro Gly Asn
                725                 730                 735
Asp Arg Leu Leu Thr Pro Asn Glu Phe Glu Ile Lys Arg Ser Val Asp
            740                 745                 750
Gly Glu Gly Tyr Asn Val Ala Gln Cys Asn Met Thr Lys Asp Trp Phe
        755                 760                 765
Leu Val Gln Met Leu Ala Asn Tyr Asn Ile Gly Tyr Gln Gly Phe Tyr
    770                 775                 780
Ile Pro Glu Ser Tyr Lys Asp Arg Met Tyr Ser Phe Phe Arg Asn Phe
785                 790                 795                 800
Gln Pro Met Ser Arg Gln Val Val Asp Gln Thr Lys Tyr Lys Asp Tyr
                805                 810                 815
Gln Glu Val Gly Ile Ile His Gln His Asn Asn Ser Gly Phe Val Gly
            820                 825                 830
Tyr Leu Ala Pro Thr Met Arg Glu Gly Gln Ala Tyr Pro Ala Asn Phe
        835                 840                 845
Pro Tyr Pro Leu Ile Gly Lys Thr Ala Val Asp Ser Ile Thr Gln Lys
    850                 855                 860
Lys Phe Leu Cys Asp Arg Thr Leu Trp Arg Ile Pro Phe Ser Ser Asn
```

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865                 870                 875                 880
Phe Met Ser Met Gly Ala Leu Thr Asp Leu Gly Gln Asn Leu Leu Tyr
                885                 890                 895
Ala Asn Ser Ala His Ala Leu Asp Met Thr Phe Glu Val Asp Pro Met
            900                 905                 910
Asp Glu Pro Thr Leu Leu Tyr Val Leu Phe Glu Val Phe Asp Val Val
        915                 920                 925
Arg Val His Gln Pro His Arg Gly Val Ile Glu Thr Val Tyr Leu Arg
    930                 935                 940
Thr Pro Phe Ser Ala Gly Asn Ala Thr Thr
945                 950
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<210> 103
<211> 2841
<212> DNA
<213> Chimpanzee Adenovirus- ChAd 26 Hexon

<400> 103
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tcggagtacc tgagtccggg tctggtgcag ttcgcccgcg ccacagacac ctacttcagt 120
ctggggaaca agtttaggaa ccccacggtg gcgcccacgc acgatgtgac caccgaccgc 180
agccagcggc tgacgctgcg cttcgtgccc gtggaccgcg aggacaacac ctactcgtac 240
aaagtgcgct acacgctggc cgtgggcgac aaccgcgtgc tggacatggc cagcacctac 300
tttgacatcc gcggcgtgct ggaccggggc cctagcttca aacccctactc cggcaccgcc 360
tacaacagcc tggctcccaa gggagcaccc aattccagcc agtgggagca aaaaaagaca 420
ggcaataaca atggaaatgg cggcactgaa tctgttacct ttggtgtagc cgccatgggc 480
ggagagaata ttacaaaaga gggtcttcaa attggaagtg atgaaactaa aaccgataac 540
aaagaaattt atgcagacaa gacctaccaa cctgagcctc aaataggaga ggagaactgg 600
caagaaacat tctcttttta tggtggtaga gctcttaaaa aagatactaa gatgaaacca 660
tgctatggct cctttgctag gcccacaaat gaaaagggag gtcaggccaa atttaaagtt 720
caagacggtg tgcagactac agaatatgac atcgacctgg ctttctttga tattccaagc 780
accggcacag ggggcaatgg tacaaatgta aatgataagc cagacatggt catgtacact 840
gaaaatgtga atttggagac gccagatact catattgtgt acaaacctgg aacttcagat 900
gacagctcta aagccaactt gtgccagcag gccatgccaa acagacccaa ctacattggt 960
ttcagagaca actttattgg gctcatgtat tacaacagta ctggcaatat gggggtgctg 1020
gctggtcagg cctctcagct gaatgctgtg gtcgacttgc aagacagaaa caccgaactg 1080
tcttaccagc tcttgctcga ctctctgggt gacagaacca ggtatttcag tatgtggaac 1140
caggcggtgg acagttatga ccctgatgtg cgcattattg aaaaccatgg tgtggaggat 1200
gaattgccaa actattgctt ccccttggat ggagctggca ctaatgctgt ataccagggt 1260
gttaaagcaa aagataacgg aaacgcagcc aatggaaact gggaacaaga cacaggcgtt 1320
tcaagtatta accagatatg caaggggaac atctatgcca tggaaatcaa cattcaagcc 1380
aacctgtgga gaagtttcct ttactcgaac gtggccctgt acctgcccga ctcttacaag 1440
tacacgccgg ccaacatcac cctgcccacc aacaccaaca cctacgatta catgaacggt 1500
cgggtggtgc ctccctcgct ggtggacgcc tacatcaaca tcggggcgcg ctggtcgctg 1560
gaccccatgg acaacgtcaa tccttcaac caccaccgca acgcgggcct gcgctaccgc 1620
tccatgctcc tgggcaacgg gcgctacgtg cccttccaca tccaggtgcc ccagaaattt 1680
ttcgccatca agagcctcct gctcctgccc gggtcctaca cctacgagtg gaacttccgc 1740
aaggacgtca acatgatcct gcagagctcc ctcggcaacg acctgcgcac ggacggggcc 1800
tccatctcct tcaccagcat caacctctac gccaccttct tccccatggc gcacaacacg 1860
gcttccacgc tcgaggccat gctgcgcaac gacaccaacg accagtcctt caacgactac 1920
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atcccctcgc gcaactgggc cgccttccgc ggctggtcct tcacgcgtct caagaccaag 2040
gaaacgccct cgctgggctc cgggttcgac ccctacttcg tctactcggg ctccatcccc 2100
tacctcgacg gcaccttcta cctcaaccac accttcaaga aggtctccat caccttcgac 2160

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tcctccgtca gctggcccgg caacgaccgg ctcctgacgc ccaacgagtt cgaaatcaag 2220
cgcaccgtcg acggcgaggg ctacaacgtg gcccagtgca acatgaccaa ggactggttc 2280
ctggtccaga tgctggccca ctacaacatc ggctaccagg gcttctacgt gcccgagggc 2340
tacaaggacc gcatgtactc cttcttccgc aacttccagc ccatgagccg ccaggtggtg 2400
gacgaggtca actacaagga ctaccaggcc gtcaccctgg cctaccagca caacaactcg 2460
ggcttcgtcg gctacctcgc gcccaccatg cgccagggcc agccctaccc cgccaactac 2520
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gtcgacccca tggatgagtc cacccttctc tatgttgtct tcgaagtctt cgacgtcgtc 2760
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<210> 104
<211> 946
<212> PRT
<213> Chimpanzee Adenovirus- ChAd 26 Hexon

<400> 104
Met Ala Thr Pro Ser Met Leu Pro Gln Trp Ala Tyr Met His Ile Ala
 1               5                  10                  15
Gly Gln Asp Ala Ser Glu Tyr Leu Ser Pro Gly Leu Val Gln Phe Ala
            20                  25                  30
Arg Ala Thr Asp Thr Tyr Phe Ser Leu Gly Asn Lys Phe Arg Asn Pro
        35                  40                  45
Thr Val Ala Pro Thr His Asp Val Thr Thr Asp Arg Ser Gln Arg Leu
    50                  55                  60
Thr Leu Arg Phe Val Pro Val Asp Arg Glu Asp Asn Thr Tyr Ser Tyr
65                  70                  75                  80
Lys Val Arg Tyr Thr Leu Ala Val Gly Asp Asn Arg Val Leu Asp Met
                85                  90                  95
Ala Ser Thr Tyr Phe Asp Ile Arg Gly Val Leu Asp Arg Gly Pro Ser
            100                 105                 110
Phe Lys Pro Tyr Ser Gly Thr Ala Tyr Asn Ser Leu Ala Pro Lys Gly
        115                 120                 125
Ala Pro Asn Ser Ser Gln Trp Glu Gln Lys Lys Thr Gly Asn Asn Asn
    130                 135                 140
Gly Asn Gly Gly Thr Glu Ser Val Thr Phe Gly Val Ala Ala Met Gly
145                 150                 155                 160
Gly Glu Asn Ile Thr Lys Glu Gly Leu Gln Ile Gly Ser Asp Glu Thr
                165                 170                 175
Lys Thr Asp Asn Lys Glu Ile Tyr Ala Asp Lys Thr Tyr Gln Pro Glu
            180                 185                 190
Pro Gln Ile Gly Glu Glu Asn Trp Gln Glu Thr Phe Ser Phe Tyr Gly
        195                 200                 205
Gly Arg Ala Leu Lys Lys Asp Thr Lys Met Lys Pro Cys Tyr Gly Ser
    210                 215                 220
Phe Ala Arg Pro Thr Asn Glu Lys Gly Gly Gln Ala Lys Phe Lys Val
225                 230                 235                 240
Gln Asp Gly Val Gln Thr Thr Glu Tyr Asp Ile Asp Leu Ala Phe Phe
                245                 250                 255
Asp Ile Pro Ser Thr Gly Thr Gly Gly Asn Gly Thr Asn Val Asn Asp
            260                 265                 270
Lys Pro Asp Met Val Met Tyr Thr Glu Asn Val Asn Leu Glu Thr Pro
        275                 280                 285
```

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Asp Thr His Ile Val Tyr Lys Pro Gly Thr Ser Asp Asp Ser Ser Lys
    290                 295                 300
Ala Asn Leu Cys Gln Gln Ala Met Pro Asn Arg Pro Asn Tyr Ile Gly
305                 310                 315                 320
Phe Arg Asp Asn Phe Ile Gly Leu Met Tyr Tyr Asn Ser Thr Gly Asn
                325                 330                 335
Met Gly Val Leu Ala Gly Gln Ala Ser Gln Leu Asn Ala Val Val Asp
            340                 345                 350
Leu Gln Asp Arg Asn Thr Glu Leu Ser Tyr Gln Leu Leu Leu Asp Ser
        355                 360                 365
Leu Gly Asp Arg Thr Arg Tyr Phe Ser Met Trp Asn Gln Ala Val Asp
    370                 375                 380
Ser Tyr Asp Pro Asp Val Arg Ile Ile Glu Asn His Gly Val Glu Asp
385                 390                 395                 400
Glu Leu Pro Asn Tyr Cys Phe Pro Leu Asp Gly Ala Gly Thr Asn Ala
                405                 410                 415
Val Tyr Gln Gly Val Lys Ala Lys Asp Asn Gly Asn Ala Ala Asn Gly
            420                 425                 430
Asn Trp Glu Gln Asp Thr Gly Val Ser Ser Ile Asn Gln Ile Cys Lys
        435                 440                 445
Gly Asn Ile Tyr Ala Met Glu Ile Asn Ile Gln Ala Asn Leu Trp Arg
    450                 455                 460
Ser Phe Leu Tyr Ser Asn Val Ala Leu Tyr Leu Pro Asp Ser Tyr Lys
465                 470                 475                 480
Tyr Thr Pro Ala Asn Ile Thr Leu Pro Thr Asn Thr Asn Thr Tyr Asp
                485                 490                 495
Tyr Met Asn Gly Arg Val Val Pro Pro Ser Leu Val Asp Ala Tyr Ile
            500                 505                 510
Asn Ile Gly Ala Arg Trp Ser Leu Asp Pro Met Asp Asn Val Asn Pro
        515                 520                 525
Phe Asn His His Arg Asn Ala Gly Leu Arg Tyr Arg Ser Met Leu Leu
    530                 535                 540
Gly Asn Gly Arg Tyr Val Pro Phe His Ile Gln Val Pro Gln Lys Phe
545                 550                 555                 560
Phe Ala Ile Lys Ser Leu Leu Leu Leu Pro Gly Ser Tyr Thr Tyr Glu
                565                 570                 575
Trp Asn Phe Arg Lys Asp Val Asn Met Ile Leu Gln Ser Ser Leu Gly
            580                 585                 590
Asn Asp Leu Arg Thr Asp Gly Ala Ser Ile Ser Phe Thr Ser Ile Asn
        595                 600                 605
Leu Tyr Ala Thr Phe Phe Pro Met Ala His Asn Thr Ala Ser Thr Leu
    610                 615                 620
Glu Ala Met Leu Arg Asn Asp Thr Asn Asp Gln Ser Phe Asn Asp Tyr
625                 630                 635                 640
Leu Ser Ala Ala Asn Met Leu Tyr Pro Ile Pro Ala Asn Ala Thr Asn
                645                 650                 655
Val Pro Ile Ser Ile Pro Ser Arg Asn Trp Ala Ala Phe Arg Gly Trp
            660                 665                 670
Ser Phe Thr Arg Leu Lys Thr Lys Glu Thr Pro Ser Leu Gly Ser Gly
        675                 680                 685
Phe Asp Pro Tyr Phe Val Tyr Ser Gly Ser Ile Pro Tyr Leu Asp Gly
    690                 695                 700
Thr Phe Tyr Leu Asn His Thr Phe Lys Lys Val Ser Ile Thr Phe Asp
705                 710                 715                 720
Ser Ser Val Ser Trp Pro Gly Asn Asp Arg Leu Leu Thr Pro Asn Glu
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```
                725                 730                 735
Phe Glu Ile Lys Arg Thr Val Asp Gly Glu Gly Tyr Asn Val Ala Gln
            740                 745                 750
Cys Asn Met Thr Lys Asp Trp Phe Leu Val Gln Met Leu Ala His Tyr
        755                 760                 765
Asn Ile Gly Tyr Gln Gly Phe Tyr Val Pro Glu Gly Tyr Lys Asp Arg
    770                 775                 780
Met Tyr Ser Phe Phe Arg Asn Phe Gln Pro Met Ser Arg Gln Val Val
785                 790                 795                 800
Asp Glu Val Asn Tyr Lys Asp Tyr Gln Ala Val Thr Leu Ala Tyr Gln
                805                 810                 815
His Asn Asn Ser Gly Phe Val Gly Tyr Leu Ala Pro Thr Met Arg Gln
            820                 825                 830
Gly Gln Pro Tyr Pro Ala Asn Tyr Pro Tyr Pro Leu Ile Gly Lys Ser
        835                 840                 845
Ala Val Thr Ser Val Thr Gln Lys Lys Phe Leu Cys Asp Arg Val Met
    850                 855                 860
Trp Arg Ile Pro Phe Ser Ser Asn Phe Met Ser Met Gly Ala Leu Thr
865                 870                 875                 880
Asp Leu Gly Gln Asn Met Leu Tyr Ala Asn Ser Ala His Ala Leu Asp
                885                 890                 895
Met Asn Phe Glu Val Asp Pro Met Asp Glu Ser Thr Leu Leu Tyr Val
            900                 905                 910
Val Phe Glu Val Phe Asp Val Val Arg Val His Gln Pro His Arg Gly
        915                 920                 925
Val Ile Glu Ala Val Tyr Leu Arg Thr Pro Phe Ser Ala Gly Asn Ala
    930                 935                 940
Thr Thr
945
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<210> 105
<211> 2838
<212> DNA
<213> Chimpanzee Adenovirus- ChAd 30 Hexon

<400> 105

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tacaactctc tggctcctaa gggagctcct aatcctagcc aatggctaga acaatcaacg 420
acagagggag aagacgatcc aactaacact acacacacat ttggaatagc ttctatgaaa 480
ggagaaaaca tcaccaaaga aggtttgcaa attggaaaag aagtaaccac tactggagat 540
aaaccaattt atgcagataa aacctttcag ccagaacccc aagtgggaga agagacttgg 600
actgatactg acgggacaaa tgaaaagttt ggcggtagaa ctcttaaaag tgctactaat 660
atgaaaccat gctatgggtc ttttgctagg cccacaaaca aacaaggcgg acaagctaaa 720
accagaaaag tagcggcagt tgatgggggg gaggaaactg aagaaccaga catcgacatg 780
gtgttttatg atgatagagg tgctacagaa gccatgatgg ctcctgaagt tgtactttat 840
gcagaaaatg taaatctgga aacaccagac acccatgtgg tgtacaaacc aggaacctct 900
gatattaatt ctcatgaaaa tttgggtcag caggctatgc caaacaggcc caattacatt 960
ggattcagag ataactttgt tggactcatg tactacaata gtactggcaa tatgggtgtg 1020
ttggcagggc aggcatcaca gctaaatgca gtagttgact tgcaagacag aaacactgag 1080
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<210> 106
<211> 945
<212> PRT
<213> Chimpanzee Adenovirus- ChAd 30 Hexon

<400> 106

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Gly Gln Asp Ala Ser Glu Tyr Leu Ser Pro Gly Leu Val Gln Phe Ala
            20                  25                  30
Arg Ala Thr Asp Thr Tyr Phe Asn Leu Gly Asn Lys Phe Arg Asn Pro
        35                  40                  45
Thr Val Ala Pro Thr His Asp Val Thr Thr Asp Arg Ser Gln Arg Leu
    50                  55                  60
Met Leu Arg Phe Val Pro Val Asp Arg Glu Asp Asn Thr Tyr Ser Tyr
65                  70                  75                  80
Lys Val Arg Tyr Thr Leu Ala Val Gly Asp Asn Arg Val Leu Asp Met
                85                  90                  95
Ala Ser Thr Phe Phe Asp Ile Arg Gly Val Leu Asp Arg Gly Pro Ser
            100                 105                 110
Phe Lys Pro Tyr Ser Gly Thr Ala Tyr Asn Ser Leu Ala Pro Lys Gly
        115                 120                 125
Ala Pro Asn Pro Ser Gln Trp Leu Glu Gln Ser Thr Thr Glu Gly Glu
    130                 135                 140
```

```
Asp Asp Pro Thr Asn Thr Thr His Thr Phe Gly Ile Ala Ser Met Lys
145                 150                 155                 160
Gly Glu Asn Ile Thr Lys Glu Gly Leu Gln Ile Gly Lys Glu Val Thr
                165                 170                 175
Thr Thr Gly Asp Lys Pro Ile Tyr Ala Asp Lys Thr Phe Gln Pro Glu
            180                 185                 190
Pro Gln Val Gly Glu Glu Thr Trp Thr Asp Thr Asp Gly Thr Asn Glu
        195                 200                 205
Lys Phe Gly Gly Arg Thr Leu Lys Ser Ala Thr Asn Met Lys Pro Cys
    210                 215                 220
Tyr Gly Ser Phe Ala Arg Pro Thr Asn Lys Gln Gly Gly Gln Ala Lys
225                 230                 235                 240
Thr Arg Lys Val Ala Ala Val Asp Gly Gly Glu Glu Thr Glu Glu Pro
                245                 250                 255
Asp Ile Asp Met Val Phe Tyr Asp Asp Arg Gly Ala Thr Glu Ala Met
            260                 265                 270
Met Ala Pro Glu Val Val Leu Tyr Ala Glu Asn Val Asn Leu Glu Thr
        275                 280                 285
Pro Asp Thr His Val Val Tyr Lys Pro Gly Thr Ser Asp Ile Asn Ser
    290                 295                 300
His Glu Asn Leu Gly Gln Gln Ala Met Pro Asn Arg Pro Asn Tyr Ile
305                 310                 315                 320
Gly Phe Arg Asp Asn Phe Val Gly Leu Met Tyr Tyr Asn Ser Thr Gly
                325                 330                 335
Asn Met Gly Val Leu Ala Gly Gln Ala Ser Gln Leu Asn Ala Val Val
            340                 345                 350
Asp Leu Gln Asp Arg Asn Thr Glu Leu Ser Tyr Gln Leu Leu Leu Asp
        355                 360                 365
Ser Leu Gly Asp Arg Thr Arg Tyr Phe Ser Met Trp Asn Gln Ala Val
    370                 375                 380
Asp Ser Tyr Asp Pro Asp Val Arg Ile Ile Glu Asn His Gly Ile Glu
385                 390                 395                 400
Asp Glu Leu Pro Asn Tyr Cys Phe Pro Leu Asp Gly Ile Gly Pro Gly
                405                 410                 415
Lys Thr Tyr Gln Gly Ile Lys Glu Lys Gln Gly Asp Glu Ala Asn Lys
            420                 425                 430
Trp Glu Gln Asp Lys Thr Tyr Ala Thr Ser Asn Glu Ile Ala Ile Gly
        435                 440                 445
Asn Asn Leu Ala Met Glu Ile Asn Ile Gln Ala Asn Leu Trp Arg Ser
    450                 455                 460
Phe Leu Tyr Ser Asn Val Ala Leu Tyr Leu Pro Asp Ala Tyr Lys Tyr
465                 470                 475                 480
Thr Pro Ala Asn Ile Thr Leu Pro Ala Asn Thr Asn Thr Tyr Glu Tyr
                485                 490                 495
Met Asn Gly Arg Val Val Ala Pro Ser Leu Val Asp Ser Tyr Ile Asn
            500                 505                 510
Ile Gly Ala Arg Trp Ser Leu Asp Pro Met Asp Asn Val Asn Pro Phe
        515                 520                 525
Asn His His Arg Asn Ala Gly Leu Arg Tyr Arg Ser Met Leu Leu Gly
    530                 535                 540
Asn Gly Arg Tyr Val Pro Phe His Ile Gln Val Pro Gln Lys Phe Phe
545                 550                 555                 560
Ala Ile Lys Asn Leu Leu Leu Leu Pro Gly Ser Tyr Thr Tyr Glu Trp
                565                 570                 575
Asn Phe Arg Lys Asp Val Asn Met Val Leu Gln Ser Ser Leu Gly Asn
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            580                 585                 590
Asp Leu Arg Thr Asp Gly Ala Ser Ile Ser Phe Thr Ser Ile Asn Leu
        595                 600                 605
Tyr Ala Thr Phe Phe Pro Met Ala His Asn Thr Ala Ser Thr Leu Glu
    610                 615                 620
Ala Met Leu Arg Asn Asp Thr Asn Asp Gln Ser Phe Asn Asp Tyr Leu
625                 630                 635                 640
Ser Ala Ala Asn Met Leu Tyr Pro Ile Pro Ala Asn Ala Thr Asn Ile
                645                 650                 655
Pro Ile Ser Ile Pro Ser Arg Asn Trp Ala Ala Phe Arg Gly Trp Ser
            660                 665                 670
Phe Thr Arg Leu Lys Thr Lys Glu Thr Pro Ser Leu Gly Ser Gly Phe
        675                 680                 685
Asp Pro Tyr Phe Val Tyr Ser Gly Ser Ile Pro Tyr Leu Asp Gly Thr
    690                 695                 700
Phe Tyr Leu Asn His Thr Phe Lys Lys Val Ser Ile Met Phe Asp Ser
705                 710                 715                 720
Ser Val Ser Trp Pro Gly Asn Asp Arg Leu Leu Thr Pro Asn Glu Phe
                725                 730                 735
Glu Ile Lys Arg Thr Val Asp Gly Glu Gly Tyr Asn Val Ala Gln Cys
            740                 745                 750
Asn Met Thr Lys Asp Trp Phe Leu Val Gln Met Leu Ala Asn Tyr Asn
        755                 760                 765
Ile Gly Tyr Gln Gly Phe Tyr Ile Pro Glu Gly Tyr Lys Asp Arg Met
    770                 775                 780
Tyr Ser Phe Phe Arg Asn Phe Gln Pro Met Ser Arg Gln Val Val Asp
785                 790                 795                 800
Glu Val Asn Tyr Lys Glu Tyr Gln Ala Val Thr Leu Ala Tyr Gln His
                805                 810                 815
Asn Asn Ser Gly Phe Val Gly Tyr Leu Ala Pro Thr Met Arg Gln Gly
            820                 825                 830
Glu Pro Tyr Pro Ala Asn Tyr Pro Tyr Pro Leu Ile Gly Thr Thr Ala
        835                 840                 845
Val Lys Ser Val Thr His Lys Lys Phe Leu Cys Asp Arg Thr Met Trp
    850                 855                 860
Arg Ile Pro Phe Ser Ser Asn Phe Met Ser Met Gly Ala Leu Thr Asp
865                 870                 875                 880
Leu Gly Gln Asn Met Leu Tyr Ala Asn Ser Ser His Ala Leu Asp Met
                885                 890                 895
Thr Phe Glu Val Asp Pro Met Asp Glu Pro Thr Leu Leu Tyr Leu Leu
            900                 905                 910
Phe Glu Val Phe Asp Val Val Arg Ala His Gln Pro His Arg Gly Val
        915                 920                 925
Ile Glu Ala Val Tyr Leu Arg Thr Pro Phe Ser Ala Gly Asn Ala Thr
    930                 935                 940
Thr
945
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<210> 107
<211> 2877
<212> DNA
<213> Chimpanzee Adenovirus- ChAd 31 Hexon

<400> 107

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tcggagtacc tgagccccgg gctggtgcag ttcgcccgcg ccaccgagag ctacttcagc 120
ctgagtaaca agtttaggaa ccccacggtg gcgcccacgc acgatgtgac caccgaccgg 180
tctcagcgcc tgacgctgcg gttcattccc gtggaccgcg aggacaccgc gtactcgtac 240
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<210> 108
<211> 958
<212> PRT
<213> Chimpanzee Adenovirus- ChAd 31 Hexon

<400> 108

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            20                  25                  30
Arg Ala Thr Glu Ser Tyr Phe Ser Leu Ser Asn Lys Phe Arg Asn Pro
        35                  40                  45
Thr Val Ala Pro Thr His Asp Val Thr Thr Asp Arg Ser Gln Arg Leu
    50                  55                  60
Thr Leu Arg Phe Ile Pro Val Asp Arg Glu Asp Thr Ala Tyr Ser Tyr
65                  70                  75                  80
Lys Ala Arg Phe Thr Leu Ala Val Gly Asp Asn Arg Val Leu Asp Met
                85                  90                  95
Ala Ser Thr Tyr Phe Asp Ile Arg Gly Val Leu Asp Arg Gly Pro Thr
            100                 105                 110
Phe Lys Pro Tyr Ser Gly Thr Ala Tyr Asn Ser Leu Ala Pro Lys Gly
        115                 120                 125
Ala Pro Asn Ser Cys Glu Trp Glu Gln Leu Glu Glu Ala Gln Ala Ala
    130                 135                 140
Val Glu Asp Glu Glu Leu Glu Asp Glu Asp Glu Glu Pro Gln Asp Glu
145                 150                 155                 160
Ala Pro Val Lys Lys Thr His Val Tyr Ala Gln Ala Pro Leu Ser Gly
                165                 170                 175
Glu Glu Ile Thr Lys Asn Gly Leu Gln Ile Gly Ser Asp Asn Thr Glu
            180                 185                 190
Ala Gln Ser Lys Pro Ile Tyr Ala Asp Pro Thr Phe Gln Pro Glu Pro
        195                 200                 205
Gln Ile Gly Glu Ser Gln Trp Asn Glu Ala Asp Ala Thr Val Ala Gly
    210                 215                 220
Gly Arg Val Leu Lys Lys Ser Thr Pro Met Lys Pro Cys Tyr Gly Ser
225                 230                 235                 240
Tyr Ala Arg Pro Thr Asn Ser Asn Gly Gly Gln Gly Val Leu Val Ala
                245                 250                 255
Asp Asp Lys Gly Val Leu Gln Ser Lys Val Glu Leu Gln Phe Phe Ser
            260                 265                 270
Asn Thr Thr Thr Leu Asn Gln Arg Glu Gly Asn Asp Thr Lys Pro Lys
        275                 280                 285
Val Val Leu Tyr Ser Glu Asp Val His Met Glu Thr Pro Asp Thr His
    290                 295                 300
Ile Ser Tyr Lys Pro Thr Lys Ser Asp Asp Asn Ser Lys Ile Met Leu
305                 310                 315                 320
Gly Gln Gln Ser Met Pro Asn Arg Pro Asn Tyr Ile Gly Phe Arg Asp
                325                 330                 335
Asn Phe Ile Gly Leu Met Tyr Tyr Asn Ser Thr Gly Asn Met Gly Val
            340                 345                 350
Leu Ala Gly Gln Ala Ser Gln Leu Asn Ala Val Val Asp Leu Gln Asp
        355                 360                 365
Arg Asn Thr Glu Leu Ser Tyr Gln Leu Leu Leu Asp Ser Met Gly Asp
    370                 375                 380
Arg Thr Arg Tyr Phe Ser Met Trp Asn Gln Ala Val Asp Ser Tyr Asp
385                 390                 395                 400
Pro Asp Val Arg Ile Ile Glu Asn His Gly Thr Glu Asp Glu Leu Pro
                405                 410                 415
Asn Tyr Cys Phe Pro Leu Gly Gly Ile Gly Val Thr Asp Thr Tyr Gln
            420                 425                 430
Ala Ile Lys Thr Asn Gly Asn Gly Gln Glu Asn Pro Thr Trp Glu Lys
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        435                 440                 445
Asp Thr Glu Phe Ala Asp Arg Asn Glu Ile Gly Val Gly Asn Asn Phe
    450                 455                 460
Ala Met Glu Ile Asn Leu Ser Ala Asn Leu Trp Arg Asn Phe Leu Tyr
465                 470                 475                 480
Ser Asn Val Ala Leu Tyr Leu Pro Asp Lys Leu Lys Tyr Asn Pro Ser
                485                 490                 495
Asn Val Asp Ile Ser Asp Asn Pro Asn Thr Tyr Asp Tyr Met Asn Lys
            500                 505                 510
Arg Val Val Ala Pro Gly Leu Val Asp Cys Tyr Ile Asn Leu Gly Ala
        515                 520                 525
Arg Trp Ser Leu Asp Tyr Met Asp Asn Val Asn Pro Phe Asn His His
    530                 535                 540
Arg Asn Ala Gly Leu Arg Tyr Arg Ser Met Leu Leu Gly Asn Gly Arg
545                 550                 555                 560
Tyr Val Pro Phe His Ile Gln Val Pro Gln Lys Phe Phe Ala Ile Lys
                565                 570                 575
Asn Leu Leu Leu Leu Pro Gly Ser Tyr Thr Tyr Glu Trp Asn Phe Arg
            580                 585                 590
Lys Asp Val Asn Met Val Leu Gln Ser Ser Leu Gly Asn Asp Leu Arg
        595                 600                 605
Val Asp Gly Ala Ser Ile Lys Phe Glu Ser Ile Cys Leu Tyr Ala Thr
    610                 615                 620
Phe Phe Pro Met Ala His Asn Thr Ala Ser Thr Leu Glu Ala Met Leu
625                 630                 635                 640
Arg Asn Asp Thr Asn Asp Gln Ser Phe Asn Asp Tyr Leu Ser Ala Ala
                645                 650                 655
Asn Met Leu Tyr Pro Ile Pro Ala Asn Ala Thr Asn Val Pro Ile Ser
            660                 665                 670
Ile Pro Ser Arg Asn Trp Ala Ala Phe Arg Gly Trp Ala Phe Thr Arg
        675                 680                 685
Leu Lys Thr Lys Glu Thr Pro Ser Leu Gly Ser Gly Phe Asp Pro Tyr
    690                 695                 700
Tyr Thr Tyr Ser Gly Ser Ile Pro Tyr Leu Asp Gly Thr Phe Tyr Leu
705                 710                 715                 720
Asn His Thr Phe Lys Lys Val Ser Val Thr Phe Asp Ser Ser Val Ser
                725                 730                 735
Trp Pro Gly Asn Asp Arg Leu Leu Thr Pro Asn Glu Phe Glu Ile Lys
            740                 745                 750
Arg Ser Val Asp Gly Glu Gly Tyr Asn Val Ala Gln Cys Asn Met Thr
        755                 760                 765
Lys Asp Trp Phe Leu Val Gln Met Leu Ala Asn Tyr Asn Ile Gly Tyr
    770                 775                 780
Gln Gly Phe Tyr Ile Pro Glu Ser Tyr Lys Asp Arg Met Tyr Ser Phe
785                 790                 795                 800
Phe Arg Asn Phe Gln Pro Met Ser Arg Gln Val Val Asp Gln Thr Lys
                805                 810                 815
Tyr Lys Asp Tyr Gln Glu Val Gly Ile Ile His Gln His Asn Asn Ser
            820                 825                 830
Gly Phe Val Gly Tyr Leu Ala Pro Thr Met Arg Glu Gly Gln Ala Tyr
        835                 840                 845
Pro Ala Asn Phe Pro Tyr Pro Leu Ile Gly Lys Thr Ala Val Asp Ser
    850                 855                 860
Ile Thr Gln Lys Lys Phe Leu Cys Asp Arg Thr Leu Trp Arg Ile Pro
865                 870                 875                 880
```

```
Phe Ser Ser Asn Phe Met Ser Met Gly Ala Leu Ser Asp Leu Gly Gln
                885                 890                 895
Asn Leu Leu Tyr Ala Asn Ser Ala His Ala Leu Asp Met Thr Phe Glu
            900                 905                 910
Val Asp Pro Met Asp Glu Pro Thr Leu Leu Tyr Val Leu Phe Glu Val
        915                 920                 925
Phe Asp Val Val Arg Val His Gln Pro His Arg Gly Val Ile Glu Thr
    930                 935                 940
Val Tyr Leu Arg Thr Pro Phe Ser Ala Gly Asn Ala Thr Thr
945                 950                 955
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<210> 109
<211> 2856
<212> DNA
<213> Chimpanzee Adenovirus- ChAd 37 Hexon

<400> 109

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cagcacaaca actctggctt tgtgggttac catgcaccca ctctccgtca gggtcaacca 2520
tacccagcta actacccata cccgcttatt ggaaccactg ctgtcaccag cgtcacccag 2580
aaaaagttct tgtgcgacag gaccatgtgg cgcatcccct tctccagcaa cttcatgtcc 2640
atgggtgccc ttaccgacct ggggcagaac atgctttatg ctaactcagc tcatgcgctg 2700
gacatgactt ttgaggtgga tcccatggat gagcccacac tgctttatct tcttttcgaa 2760
gtcttcgacg tggtcagagt gcaccagcca caccgcggcg tcatcgaggc cgtctacctg 2820
cgcacaccgt tctcggccgg caacgccacc acataa                           2856
```

<210> 110
<211> 951
<212> PRT
<213> Chimpanzee Adenovirus- ChAd 37 Hexon

<400> 110

```
Met Ala Thr Pro Ser Met Leu Pro Gln Trp Ala Tyr Met His Ile Ala
 1               5                  10                  15
Gly Gln Asp Ala Ser Glu Tyr Leu Ser Pro Gly Leu Val Gln Phe Ala
            20                  25                  30
Arg Ala Thr Asp Thr Tyr Phe Asn Leu Gly Asn Lys Phe Arg Asn Pro
        35                  40                  45
Thr Val Ala Pro Thr His Asp Val Thr Thr Asp Arg Ser Gln Arg Leu
    50                  55                  60
Met Leu Arg Phe Val Pro Val Asp Arg Glu Asp Asn Thr Tyr Ser Tyr
65                  70                  75                  80
Lys Val Arg Tyr Thr Leu Ala Val Gly Asp Asn Arg Val Leu Asp Met
                85                  90                  95
Ala Ser Thr Phe Phe Asp Ile Arg Gly Val Leu Asp Arg Gly Pro Ser
            100                 105                 110
Phe Lys Pro Tyr Ser Gly Thr Ala Tyr Asn Ser Leu Ala Pro Lys Gly
        115                 120                 125
Ala Pro Asn Thr Cys Gln Trp Ile Ala Lys Gly Ala Pro Val Thr Asp
    130                 135                 140
Gln Asp Asn Glu Glu Gln Glu Leu Thr Asp Val Thr Tyr Ala Phe Gly
145                 150                 155                 160
Asn Ala Pro Val Gln Ala Glu Ala Lys Ile Thr Lys Asp Gly Leu Pro
                165                 170                 175
Val Gly Leu Glu Ile Thr Glu Asp Glu Gln Lys Ser Ile Tyr Ala Asp
            180                 185                 190
Lys Leu Tyr Gln Pro Glu Pro Gln Ile Gly Asp Glu Gln Trp His Asp
        195                 200                 205
Thr Thr Gly Thr Asn Glu Gln Tyr Gly Gly Arg Ala Leu Lys Pro Ala
    210                 215                 220
Thr Asn Met Lys Pro Cys Tyr Gly Ser Phe Ala Arg Pro Thr Asn Lys
225                 230                 235                 240
Lys Gly Gly Gln Ala Lys Thr Arg Lys Ile Glu Lys Glu Glu Asn Gly
                245                 250                 255
Val Lys Thr Val Thr Glu Glu Ala Asp Ile Asp Met Asp Phe Tyr Asp
            260                 265                 270
Leu Arg Ser Gln Arg Ala Asn Phe Asp Pro Lys Ile Val Leu Tyr Ser
        275                 280                 285
Glu Asn Val Asn Leu Glu Thr Pro Asp Thr His Ile Val Tyr Lys Pro
```

```
    290                 295                 300
Gly Thr Asp Glu Thr Ser Ser Ser Val Asn Leu Gly Gln Gln Ala Met
305                 310                 315                 320
Pro Asn Arg Pro Asn Tyr Ile Gly Phe Arg Asp Asn Phe Ile Gly Leu
                325                 330                 335
Met Phe Tyr Asn Ser Thr Gly Asn Met Gly Val Leu Ala Gly Gln Ala
            340                 345                 350
Ser Gln Leu Asn Ala Val Val Asp Leu Gln Asp Arg Asn Thr Glu Leu
        355                 360                 365
Ser Tyr Gln Leu Leu Leu Asp Ser Leu Gly Asp Arg Thr Arg Tyr Phe
    370                 375                 380
Ser Met Trp Asn Gln Ala Val Asp Ser Tyr Asp Pro Asp Val Arg Ile
385                 390                 395                 400
Ile Glu Asn His Gly Val Glu Asp Glu Leu Pro Asn Tyr Cys Phe Pro
                405                 410                 415
Leu Asp Gly Val Gly Pro Ile Thr Gly Thr Tyr Gln Gly Val Glu Pro
            420                 425                 430
Asp Gly Asn Asn Gly Asn Trp Lys Lys Asn Thr Asn Ile Asn Gly Ala
        435                 440                 445
Asn Glu Ile Gly Lys Gly Asn Asn Tyr Ala Met Glu Ile Asn Leu Gln
    450                 455                 460
Ala Asn Leu Trp Arg Ser Phe Leu Tyr Ser Asn Val Ala Leu Tyr Leu
465                 470                 475                 480
Pro Asp Gly Tyr Lys Tyr Thr Pro Ala Asn Val Thr Leu Pro Glu Asn
                485                 490                 495
Lys Asn Thr Tyr Gly Tyr Ile Asn Gly Arg Val Val Ser Pro Ser Leu
            500                 505                 510
Val Asp Ser Tyr Ile Asn Ile Gly Ala Arg Trp Ser Leu Asp Leu Met
        515                 520                 525
Asp Asn Val Asn Pro Phe Asn His His Arg Asn Ala Gly Leu Arg Tyr
    530                 535                 540
Arg Ser Met Leu Leu Gly Asn Gly Arg Tyr Val Pro Phe His Ile Gln
545                 550                 555                 560
Val Pro Gln Lys Ile Phe Ala Val Lys Asn Leu Leu Leu Leu Pro Gly
                565                 570                 575
Ser Tyr Thr Tyr Glu Trp Asn Phe Arg Lys Asp Val Asn Met Val Leu
            580                 585                 590
Gln Ser Ser Leu Gly Asn Asp Leu Arg Thr Asp Gly Ala Ser Ile Ser
        595                 600                 605
Phe Thr Ser Ile Asn Leu Tyr Ala Thr Phe Phe Pro Met Ala His Asn
    610                 615                 620
Thr Ala Ser Thr Leu Glu Ala Met Leu Arg Asn Asp Thr Asn Asp Gln
625                 630                 635                 640
Ser Phe Asn Asp Tyr Leu Ser Ala Ala Asn Met Leu Tyr Pro Ile Pro
                645                 650                 655
Ala Asn Ala Thr Asn Ile Pro Ile Ser Ile Pro Ser Arg Asn Trp Ala
            660                 665                 670
Ala Phe Arg Gly Trp Ser Phe Thr Arg Leu Lys Thr Lys Glu Thr Pro
        675                 680                 685
Ser Leu Gly Ser Gly Phe Asp Pro Tyr Phe Val Tyr Ser Gly Ser Ile
    690                 695                 700
Pro Tyr Leu Asp Gly Thr Phe Tyr Leu Asn His Thr Phe Lys Lys Val
705                 710                 715                 720
Ser Ile Met Phe Asp Ser Ser Val Ser Trp Pro Gly Asn Asp Arg Leu
                725                 730                 735
```

```
Leu Thr Pro Asn Glu Phe Glu Ile Lys Arg Thr Val Asp Gly Glu Gly
            740                 745                 750
Tyr Asn Val Ala Gln Cys Asn Met Thr Lys Asp Trp Phe Leu Val Gln
        755                 760                 765
Met Leu Ala Asn Tyr Asn Ile Gly Tyr Gln Gly Phe Tyr Ile Pro Glu
    770                 775                 780
Gly Tyr Lys Asp Arg Met Tyr Ser Phe Phe Arg Asn Phe Gln Pro Met
785                 790                 795                 800
Ser Arg Gln Val Val Asp Glu Ile Asn Tyr Lys Glu Tyr Gln Ala Val
                805                 810                 815
Thr Leu Ala Tyr Gln His Asn Asn Ser Gly Phe Val Gly Tyr His Ala
            820                 825                 830
Pro Thr Leu Arg Gln Gly Gln Pro Tyr Pro Ala Asn Tyr Pro Tyr Pro
        835                 840                 845
Leu Ile Gly Thr Thr Ala Val Thr Ser Val Thr Gln Lys Lys Phe Leu
    850                 855                 860
Cys Asp Arg Thr Met Trp Arg Ile Pro Phe Ser Ser Asn Phe Met Ser
865                 870                 875                 880
Met Gly Ala Leu Thr Asp Leu Gly Gln Asn Met Leu Tyr Ala Asn Ser
                885                 890                 895
Ala His Ala Leu Asp Met Thr Phe Glu Val Asp Pro Met Asp Glu Pro
            900                 905                 910
Thr Leu Leu Tyr Leu Leu Phe Glu Val Phe Asp Val Val Arg Val His
        915                 920                 925
Gln Pro His Arg Gly Val Ile Glu Ala Val Tyr Leu Arg Thr Pro Phe
    930                 935                 940
Ser Ala Gly Asn Ala Thr Thr
945                 950
```

<210> 111
<211> 2817
<212> DNA
<213> Chimpanzee Adenovirus- ChAd 38 Hexon

<400> 111
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atggccaccc catcgatgct gccccagtgg gcgtacatgc acatcgccgg acaggacgct 60
tcggagtacc tgagtccggg tctggtgcag ttcgcccgcg ccacagacac ctacttcagt 120
ctggggaaca agtttaggaa ccccacggtg gcgcccacgc acgatgtgac caccgaccgc 180
agccagcggc tgacgctgcg cttcgtgccc gtggaccgcg aggacaacac ctactcgtac 240
aaagtgcgct acacgctggc cgtgggcgac aaccgcgtgc tggacatggc cagcacctac 300
tttgacatcc gcggcgtgct ggaccggggc cctagcttca aaccctactc cggcaccgcc 360
tacaacgccc tggcccctaa agccgctcct aatcctagcc agtgggagga aaccactact 420
ggaacggatg gaaatgctgc tactacaact acacatagtt ttggcctggc tgctatgaaa 480
ggggacaata ttacatctga cggtttgcaa ataggaacag atgctacttc tggagaggaa 540
aaacccatct atgcagataa actgtaccag ccagaacccc aaatagggga agagtcatgg 600
actgatactg atggaaccaa tgaaaaattc ggaggaagag tccttaaaaa ggacacaagc 660
atgaaaccct gctacgggtc atttgccaaa ccaaccaata acaaaggtgg tcaagcaaaa 720
caaaaggcaa ctgaaggaac cgctgtagaa tatgatgtag acatgaactt ttttgatggt 780
agagatgcag ctgctaactt tactccagaa gtagtgttgt atgctgaaaa tgtggatttg 840
gaaactccag atacacatat tgtatacaaa ccaggaacct cagatgtgag ttcccatgtt 900
aatttgggac agcaagccat gcccaacaga cccaactaca ttggtttcag agacaacttt 960
attggtctca tgtattacaa cagcactggc aatatggggg tgctggccgg tcaggcttct 1020
cagctgaatg ctgtggttga cttgcaagac agaaacactg aactgtccta ccagctgttg 1080
cttgactctt tgggtgacag aactcggtat ttcagtatgt ggaatcaggc ggtggacagc 1140
```

```
tatgatcctg atgtgcgcat cattgaaaat catggtatag aagatgagct tcccaactat 1200
tgctttccta ttgacgctgt gggtattact agaacttatc aaggtatcaa aacgcaaaat 1260
ggtcaaacta caacttggga aaaggacacc agtgttagta cggccaatga aataggcatt 1320
ggcaacaatc ttgccatgga aatcaacatc caagccaacc tgtggaggaa cttcctctac 1380
gccaacgtgg ccctgtacct gcccgattct tacaagtaca caccggccaa cgtcaccctg 1440
cccaccaata ccaacaccta cgattacatg aacggccggg tggtggcgcc ctcgctggtg 1500
gacgcctaca tcaacatcgg ggcgcgctgg tcgctggacc ccatggataa cgtgaatccc 1560
ttcaaccacc accgcaacgc ggggctgcgc taccgctcca tgctcctggg caacgggcgc 1620
tacgtgccct tccacatcca ggtgccccag aaatttttcg ccatcaagag cctcctgctc 1680
ctgcccgggt cctacaccta cgagtggaac ttccgcaagg acgtcaacat gatcctgcag 1740
agctccctcg gcaacgacct gcgcacggac ggggcctcca tctccttcac cagcatcaac 1800
ctctacgcca ccttcttccc catggcgcac aacacggcct ccacgctcga ggccatgctg 1860
cgcaacgaca ccaacgacca gtccttcaac gactacctct cggcggccaa catgctctac 1920
cccatcccgg ccaacgccac caacgtgccc atctccatcc cctcgcgcaa ctgggccgcc 1980
ttccgcggct ggtccttcac gcgcctcaag accaaggaga cgccctcgct gggctccggg 2040
ttcgacccct acttcgtcta ctcgggctcc atcccctacc tcgacggcac cttctacctc 2100
aaccacacct tcaagaaggt ctccatcacc ttcgactcct ccgtcagctg gcccggcaac 2160
gaccggctcc tgacgcccaa cgagttcgaa atcaagcgca ccgtcgacgg cgagggctac 2220
aacgtggccc agtgcaacat gaccaaggac tggttcctgg tccagatgct ggcccactac 2280
aacatcggct accagggctt ctacgtgccc gagggctaca aggaccgcat gtactccttc 2340
ttccgcaact tccaacccat gagccgccag gtggtggacg aggtcaacta caaggactac 2400
caggccgtca ccctggccta ccagcacaac aactcgggct tcgtcggcta cctcgcgccc 2460
accatgcgcc agggccagcc ctaccccgcc aactacccct acccgctcat cggcaagagc 2520
gccgtcacca gcgtcaccca gaaaaagttc ctctgcgaca gggtcatgtg gcgcatcccc 2580
ttctccagca acttcatgtc catgggcgcg ctcaccgacc tcggccagaa catgctctat 2640
gccaactccg cccacgcgct agacatgaat ttcgaagtcg accccatgga tgagtccacc 2700
cttctctatg ttgtcttcga agtcttcgac gtcgtccgag tgcaccagcc ccaccgcggc 2760
gtcatcgagg ccgtctacct gcgcacccca ttctcggccg gtaacgccac cacctaa    2817
```

<210> 112
<211> 938
<212> PRT
<213> Chimpanzee Adenovirus- ChAd 38 Hexon

<400> 112

```
Met Ala Thr Pro Ser Met Leu Pro Gln Trp Ala Tyr Met His Ile Ala
 1               5                  10                  15
Gly Gln Asp Ala Ser Glu Tyr Leu Ser Pro Gly Leu Val Gln Phe Ala
            20                  25                  30
Arg Ala Thr Asp Thr Tyr Phe Ser Leu Gly Asn Lys Phe Arg Asn Pro
        35                  40                  45
Thr Val Ala Pro Thr His Asp Val Thr Thr Asp Arg Ser Gln Arg Leu
    50                  55                  60
Thr Leu Arg Phe Val Pro Val Asp Arg Glu Asp Asn Thr Tyr Ser Tyr
65                  70                  75                  80
Lys Val Arg Tyr Thr Leu Ala Val Gly Asp Asn Arg Val Leu Asp Met
                85                  90                  95
Ala Ser Thr Tyr Phe Asp Ile Arg Gly Val Leu Asp Arg Gly Pro Ser
            100                 105                 110
Phe Lys Pro Tyr Ser Gly Thr Ala Tyr Asn Ala Leu Ala Pro Lys Ala
        115                 120                 125
Ala Pro Asn Pro Ser Gln Trp Glu Glu Thr Thr Thr Gly Thr Asp Gly
    130                 135                 140
Asn Ala Ala Thr Thr Thr Thr His Ser Phe Gly Leu Ala Ala Met Lys
145                 150                 155                 160
```

```
Gly Asp Asn Ile Thr Ser Asp Gly Leu Gln Ile Gly Thr Asp Ala Thr
                165                 170                 175
Ser Gly Glu Glu Lys Pro Ile Tyr Ala Asp Lys Leu Tyr Gln Pro Glu
            180                 185                 190
Pro Gln Ile Gly Glu Glu Ser Trp Thr Asp Thr Asp Gly Thr Asn Glu
        195                 200                 205
Lys Phe Gly Gly Arg Val Leu Lys Lys Asp Thr Ser Met Lys Pro Cys
    210                 215                 220
Tyr Gly Ser Phe Ala Lys Pro Thr Asn Asn Lys Gly Gly Gln Ala Lys
225                 230                 235                 240
Gln Lys Ala Thr Glu Gly Thr Ala Val Glu Tyr Asp Val Asp Met Asn
                245                 250                 255
Phe Phe Asp Gly Arg Asp Ala Ala Ala Asn Phe Thr Pro Glu Val Val
            260                 265                 270
Leu Tyr Ala Glu Asn Val Asp Leu Glu Thr Pro Asp Thr His Ile Val
        275                 280                 285
Tyr Lys Pro Gly Thr Ser Asp Val Ser Ser His Val Asn Leu Gly Gln
    290                 295                 300
Gln Ala Met Pro Asn Arg Pro Asn Tyr Ile Gly Phe Arg Asp Asn Phe
305                 310                 315                 320
Ile Gly Leu Met Tyr Tyr Asn Ser Thr Gly Asn Met Gly Val Leu Ala
                325                 330                 335
Gly Gln Ala Ser Gln Leu Asn Ala Val Val Asp Leu Gln Asp Arg Asn
            340                 345                 350
Thr Glu Leu Ser Tyr Gln Leu Leu Leu Asp Ser Leu Gly Asp Arg Thr
        355                 360                 365
Arg Tyr Phe Ser Met Trp Asn Gln Ala Val Asp Ser Tyr Asp Pro Asp
    370                 375                 380
Val Arg Ile Ile Glu Asn His Gly Ile Glu Asp Glu Leu Pro Asn Tyr
385                 390                 395                 400
Cys Phe Pro Ile Asp Ala Val Gly Ile Thr Arg Thr Tyr Gln Gly Ile
                405                 410                 415
Lys Thr Gln Asn Gly Gln Thr Thr Thr Trp Glu Lys Asp Thr Ser Val
            420                 425                 430
Ser Thr Ala Asn Glu Ile Gly Ile Gly Asn Asn Leu Ala Met Glu Ile
        435                 440                 445
Asn Ile Gln Ala Asn Leu Trp Arg Asn Phe Leu Tyr Ala Asn Val Ala
    450                 455                 460
Leu Tyr Leu Pro Asp Ser Tyr Lys Tyr Thr Pro Ala Asn Val Thr Leu
465                 470                 475                 480
Pro Thr Asn Thr Asn Thr Tyr Asp Tyr Met Asn Gly Arg Val Val Ala
                485                 490                 495
Pro Ser Leu Val Asp Ala Tyr Ile Asn Ile Gly Ala Arg Trp Ser Leu
            500                 505                 510
Asp Pro Met Asp Asn Val Asn Pro Phe Asn His His Arg Asn Ala Gly
        515                 520                 525
Leu Arg Tyr Arg Ser Met Leu Leu Gly Asn Gly Arg Tyr Val Pro Phe
    530                 535                 540
His Ile Gln Val Pro Gln Lys Phe Phe Ala Ile Lys Ser Leu Leu Leu
545                 550                 555                 560
Leu Pro Gly Ser Tyr Thr Tyr Glu Trp Asn Phe Arg Lys Asp Val Asn
                565                 570                 575
Met Ile Leu Gln Ser Ser Leu Gly Asn Asp Leu Arg Thr Asp Gly Ala
            580                 585                 590
Ser Ile Ser Phe Thr Ser Ile Asn Leu Tyr Ala Thr Phe Phe Pro Met
```

```
        595                 600                 605
Ala His Asn Thr Ala Ser Thr Leu Glu Ala Met Leu Arg Asn Asp Thr
    610                 615                 620
Asn Asp Gln Ser Phe Asn Asp Tyr Leu Ser Ala Ala Asn Met Leu Tyr
625                 630                 635                 640
Pro Ile Pro Ala Asn Ala Thr Asn Val Pro Ile Ser Ile Pro Ser Arg
                645                 650                 655
Asn Trp Ala Ala Phe Arg Gly Trp Ser Phe Thr Arg Leu Lys Thr Lys
            660                 665                 670
Glu Thr Pro Ser Leu Gly Ser Gly Phe Asp Pro Tyr Phe Val Tyr Ser
        675                 680                 685
Gly Ser Ile Pro Tyr Leu Asp Gly Thr Phe Tyr Leu Asn His Thr Phe
    690                 695                 700
Lys Lys Val Ser Ile Thr Phe Asp Ser Ser Val Ser Trp Pro Gly Asn
705                 710                 715                 720
Asp Arg Leu Leu Thr Pro Asn Glu Phe Glu Ile Lys Arg Thr Val Asp
                725                 730                 735
Gly Glu Gly Tyr Asn Val Ala Gln Cys Asn Met Thr Lys Asp Trp Phe
            740                 745                 750
Leu Val Gln Met Leu Ala His Tyr Asn Ile Gly Tyr Gln Gly Phe Tyr
        755                 760                 765
Val Pro Glu Gly Tyr Lys Asp Arg Met Tyr Ser Phe Phe Arg Asn Phe
    770                 775                 780
Gln Pro Met Ser Arg Gln Val Val Asp Glu Val Asn Tyr Lys Asp Tyr
785                 790                 795                 800
Gln Ala Val Thr Leu Ala Tyr Gln His Asn Asn Ser Gly Phe Val Gly
                805                 810                 815
Tyr Leu Ala Pro Thr Met Arg Gln Gly Gln Pro Tyr Pro Ala Asn Tyr
            820                 825                 830
Pro Tyr Pro Leu Ile Gly Lys Ser Ala Val Thr Ser Val Thr Gln Lys
        835                 840                 845
Lys Phe Leu Cys Asp Arg Val Met Trp Arg Ile Pro Phe Ser Ser Asn
    850                 855                 860
Phe Met Ser Met Gly Ala Leu Thr Asp Leu Gly Gln Asn Met Leu Tyr
865                 870                 875                 880
Ala Asn Ser Ala His Ala Leu Asp Met Asn Phe Glu Val Asp Pro Met
                885                 890                 895
Asp Glu Ser Thr Leu Leu Tyr Val Val Phe Glu Val Phe Asp Val Val
            900                 905                 910
Arg Val His Gln Pro His Arg Gly Val Ile Glu Ala Val Tyr Leu Arg
        915                 920                 925
Thr Pro Phe Ser Ala Gly Asn Ala Thr Thr
    930                 935
```

<210> 113
<211> 2781
<212> DNA
<213> Chimpanzee Adenovirus- ChAd 44 Hexon

<400> 113
atggccaccc catcgatgct gccccagtgg gcgtacatgc acatcgccgg acaggacgct 60
tcggagtacc tgagtccggg tctggtgcag ttcgcccgcg ccacagacac ctacttcagt 120
ctggggaaca agtttaggaa ccccacggtg gcgcccacgc acgatgtgac caccgaccgc 180
agccagcggc tgacgctgcg cttcgtgccc gtggaccgcg aggacaacac ctactcgtac 240

```
aaagtgcgct acacgctggc cgtgggcgac aaccgcgtgc tggacatggc cagcacctac 300
tttgacatcc gcggcgtgct ggaccggggc cctagcttca aaccctactc cggcaccgcc 360
tacaacagcc tggcccccaa gggagcgccc aatcccagcc agtgggaaca aactgaaacc 420
aatgttaata aaacacacac cttcggaatg gcagccatga aaggagaggc tattgacaaa 480
aatggtctgc aaattggaac tgacgctgcg gatcaggata aaccaattta tgcagataaa 540
acattccagc ctgaacctca agtaggagag gaagactgga ttgacaaagc agatttttat 600
ggcggaagag ctcttaaaaa agataccaag atgaaaccat gctatggctc atttgccaaa 660
cctacaaatg tcaagggagg acaggcaacg cccaggacta aagcagatgg aactactgag 720
cctgatattg acatgaactt ctttgaccca accactatta acacaccaga tgtagtgttg 780
tatgctgaaa atgttgattt gcaaactcca gacacccata tagtttacaa agcaggaact 840
tcagatgaca gttctgaggt caatttggct cagcaagcta tgcctaacag gcccaactac 900
attggtttca gagacaactt tatcggactt atgtattaca atagcactgg caatatgggt 960
gtgctcgctg gtcaggcttc ccagctaaat gctgtggtgg acttgcaaga cagaaacacc 1020
gagctgtcct accagctctt gcttgactct ctgggtgaca gaaccaggta tttcagtatg 1080
tggaatcagg cggtggacag ctatgatcct gatgtgcgca ttattgaaaa ccatggtgtg 1140
gaggatgaac tgccaaacta ttgctttcct ttggatggtg tgggcactaa taccgcatac 1200
caaggcgtta aagttaagac aactaatgga aacgacacgt gggaaaaaga tgaaactgtt 1260
tatgagttta atcaaattgg aaaggggat atctatgcta tggaaatcaa cattcaagcc 1320
aacctgtgga gaagttttct ctactcgaac gtggccctgt acctgcccga ttcttacaag 1380
tacacgccgg ccaacgtcac cctgcccacc aacaccaaca cctacgatta catgaacggg 1440
agagtggtgc ctccctcgct ggtggacgcc tacatcaaca tcggggcgcg ctggtcgctg 1500
gaccccatgg acaacgtgaa ccccttcaac caccaccgca acgcggggct gcgctaccgc 1560
tccatgctcc tgggcaacgg gcgcttcgtg cccttccaca tccaggtgcc ccagaaattt 1620
ttcgccatca agagcctcct gctcctgcca gggtcctaca cctacgagtg gaacttccgc 1680
aaggacgtca acatgatcct gcagagctcc ctcggcaacg acctgcgcac ggacggggcc 1740
tccatctcct tcaccagtat caacctctac gccaccttct tccccatggc gcacaacacg 1800
gcctccacgc tcgaggccat gctgcgcaac gacaccaacg accagtcctt caacgactac 1860
ctctcggcgg ccaacatgct ctaccccatc ccggccaacg ccaccaacgt gcccatctcc 1920
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gagacgccct cgctgggctc cgggttcgac ccctacttcg tctactcggg ctccatcccc 2040
tacctcgacg gcaccttcta cctcaaccac accttcaaga aggtctccat caccttcgac 2100
tcctccgtca gctggcccgg caacgaccgc ctcctgacgc ccaacgagtt cgaaatcaag 2160
cgcaccgtcg acggagaggg gtacaacgtg gcccagtgca acatgaccaa ggactggttc 2220
ctggtccaga tgctggccca ctacaacatc ggctaccagg gcttctacgt gcccgagggc 2280
tacaaggacc gcatgtactc cttcttccgc aacttccagc ccatgagccg ccaggtggtg 2340
gacgaggtca actacaagga ctaccaggcc gtcaccctgg cctaccagca caacaactcg 2400
ggcttcgtcg gctacctcgc gcccaccatg cgccagggcc agccctaccc cgccaactac 2460
ccgtacccgc tcatcggcaa gagcgccgtc accagcgtca cccagaaaaa gttcctctgc 2520
gacagggtca tgtggcgcat ccccttctcc agcaacttca tgtccatggg cgcgctcacc 2580
gacctcggcc agaacatgct ctatgccaac tccgcccacg cgctagacat gaatttcgaa 2640
gtcgacccca tggatgagtc cacccttctc tatgttgtct tcgaagtctt cgacgtcgtc 2700
cgagtgcacc agccccaccg cggcgtcatc gaggccgtct acctgcgcac ccccttctcg 2760
gccggtaacg ccaccaccta a                                           2781
```

<210> 114
<211> 926
<212> PRT
<213> Chimpanzee Adenovirus- ChAd 44 Hexon

<400> 114

```
Met Ala Thr Pro Ser Met Leu Pro Gln Trp Ala Tyr Met His Ile Ala
 1               5                  10                  15
Gly Gln Asp Ala Ser Glu Tyr Leu Ser Pro Gly Leu Val Gln Phe Ala
            20                  25                  30
Arg Ala Thr Asp Thr Tyr Phe Ser Leu Gly Asn Lys Phe Arg Asn Pro
```

```
        35                  40                  45
Thr Val Ala Pro Thr His Asp Val Thr Thr Asp Arg Ser Gln Arg Leu
    50                  55                  60
Thr Leu Arg Phe Val Pro Val Asp Arg Glu Asp Asn Thr Tyr Ser Tyr
65                  70                  75                  80
Lys Val Arg Tyr Thr Leu Ala Val Gly Asp Asn Arg Val Leu Asp Met
                85                  90                  95
Ala Ser Thr Tyr Phe Asp Ile Arg Gly Val Leu Asp Arg Gly Pro Ser
            100                 105                 110
Phe Lys Pro Tyr Ser Gly Thr Ala Tyr Asn Ser Leu Ala Pro Lys Gly
        115                 120                 125
Ala Pro Asn Pro Ser Gln Trp Glu Gln Thr Glu Thr Asn Val Asn Lys
    130                 135                 140
Thr His Thr Phe Gly Met Ala Ala Met Lys Gly Glu Ala Ile Asp Lys
145                 150                 155                 160
Asn Gly Leu Gln Ile Gly Thr Asp Ala Ala Asp Gln Asp Lys Pro Ile
                165                 170                 175
Tyr Ala Asp Lys Thr Phe Gln Pro Glu Pro Gln Val Gly Glu Glu Asp
            180                 185                 190
Trp Ile Asp Lys Ala Asp Phe Tyr Gly Gly Arg Ala Leu Lys Lys Asp
        195                 200                 205
Thr Lys Met Lys Pro Cys Tyr Gly Ser Phe Ala Lys Pro Thr Asn Val
    210                 215                 220
Lys Gly Gly Gln Ala Thr Pro Arg Thr Lys Ala Asp Gly Thr Thr Glu
225                 230                 235                 240
Pro Asp Ile Asp Met Asn Phe Phe Asp Pro Thr Thr Ile Asn Thr Pro
                245                 250                 255
Asp Val Val Leu Tyr Ala Glu Asn Val Asp Leu Gln Thr Pro Asp Thr
            260                 265                 270
His Ile Val Tyr Lys Ala Gly Thr Ser Asp Asp Ser Ser Glu Val Asn
        275                 280                 285
Leu Ala Gln Gln Ala Met Pro Asn Arg Pro Asn Tyr Ile Gly Phe Arg
    290                 295                 300
Asp Asn Phe Ile Gly Leu Met Tyr Tyr Asn Ser Thr Gly Asn Met Gly
305                 310                 315                 320
Val Leu Ala Gly Gln Ala Ser Gln Leu Asn Ala Val Val Asp Leu Gln
                325                 330                 335
Asp Arg Asn Thr Glu Leu Ser Tyr Gln Leu Leu Leu Asp Ser Leu Gly
            340                 345                 350
Asp Arg Thr Arg Tyr Phe Ser Met Trp Asn Gln Ala Val Asp Ser Tyr
        355                 360                 365
Asp Pro Asp Val Arg Ile Ile Glu Asn His Gly Val Glu Asp Glu Leu
    370                 375                 380
Pro Asn Tyr Cys Phe Pro Leu Asp Gly Val Gly Thr Asn Thr Ala Tyr
385                 390                 395                 400
Gln Gly Val Lys Val Lys Thr Thr Asn Gly Asn Asp Thr Trp Glu Lys
                405                 410                 415
Asp Glu Thr Val Tyr Glu Phe Asn Gln Ile Gly Lys Gly Asp Ile Tyr
            420                 425                 430
Ala Met Glu Ile Asn Ile Gln Ala Asn Leu Trp Arg Ser Phe Leu Tyr
        435                 440                 445
Ser Asn Val Ala Leu Tyr Leu Pro Asp Ser Tyr Lys Tyr Thr Pro Ala
    450                 455                 460
Asn Val Thr Leu Pro Thr Asn Thr Asn Thr Tyr Asp Tyr Met Asn Gly
465                 470                 475                 480
```

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Arg Val Val Pro Pro Ser Leu Val Asp Ala Tyr Ile Asn Ile Gly Ala
                485                 490                 495
Arg Trp Ser Leu Asp Pro Met Asp Asn Val Asn Pro Phe Asn His His
            500                 505                 510
Arg Asn Ala Gly Leu Arg Tyr Arg Ser Met Leu Leu Gly Asn Gly Arg
        515                 520                 525
Phe Val Pro Phe His Ile Gln Val Pro Gln Lys Phe Phe Ala Ile Lys
    530                 535                 540
Ser Leu Leu Leu Leu Pro Gly Ser Tyr Thr Tyr Glu Trp Asn Phe Arg
545                 550                 555                 560
Lys Asp Val Asn Met Ile Leu Gln Ser Ser Leu Gly Asn Asp Leu Arg
                565                 570                 575
Thr Asp Gly Ala Ser Ile Ser Phe Thr Ser Ile Asn Leu Tyr Ala Thr
            580                 585                 590
Phe Phe Pro Met Ala His Asn Thr Ala Ser Thr Leu Glu Ala Met Leu
        595                 600                 605
Arg Asn Asp Thr Asn Asp Gln Ser Phe Asn Asp Tyr Leu Ser Ala Ala
    610                 615                 620
Asn Met Leu Tyr Pro Ile Pro Ala Asn Ala Thr Asn Val Pro Ile Ser
625                 630                 635                 640
Ile Pro Ser Arg Asn Trp Ala Ala Phe Arg Gly Trp Ser Phe Thr Arg
                645                 650                 655
Leu Lys Thr Lys Glu Thr Pro Ser Leu Gly Ser Gly Phe Asp Pro Tyr
            660                 665                 670
Phe Val Tyr Ser Gly Ser Ile Pro Tyr Leu Asp Gly Thr Phe Tyr Leu
        675                 680                 685
Asn His Thr Phe Lys Lys Val Ser Ile Thr Phe Asp Ser Ser Val Ser
    690                 695                 700
Trp Pro Gly Asn Asp Arg Leu Leu Thr Pro Asn Glu Phe Glu Ile Lys
705                 710                 715                 720
Arg Thr Val Asp Gly Glu Gly Tyr Asn Val Ala Gln Cys Asn Met Thr
                725                 730                 735
Lys Asp Trp Phe Leu Val Gln Met Leu Ala His Tyr Asn Ile Gly Tyr
            740                 745                 750
Gln Gly Phe Tyr Val Pro Glu Gly Tyr Lys Asp Arg Met Tyr Ser Phe
        755                 760                 765
Phe Arg Asn Phe Gln Pro Met Ser Arg Gln Val Val Asp Glu Val Asn
    770                 775                 780
Tyr Lys Asp Tyr Gln Ala Val Thr Leu Ala Tyr Gln His Asn Asn Ser
785                 790                 795                 800
Gly Phe Val Gly Tyr Leu Ala Pro Thr Met Arg Gln Gly Gln Pro Tyr
                805                 810                 815
Pro Ala Asn Tyr Pro Tyr Pro Leu Ile Gly Lys Ser Ala Val Thr Ser
            820                 825                 830
Val Thr Gln Lys Lys Phe Leu Cys Asp Arg Val Met Trp Arg Ile Pro
        835                 840                 845
Phe Ser Ser Asn Phe Met Ser Met Gly Ala Leu Thr Asp Leu Gly Gln
    850                 855                 860
Asn Met Leu Tyr Ala Asn Ser Ala His Ala Leu Asp Met Asn Phe Glu
865                 870                 875                 880
Val Asp Pro Met Asp Glu Ser Thr Leu Leu Tyr Val Val Phe Glu Val
                885                 890                 895
Phe Asp Val Val Arg Val His Gln Pro His Arg Gly Val Ile Glu Ala
            900                 905                 910
Val Tyr Leu Arg Thr Pro Phe Ser Ala Gly Asn Ala Thr Thr
```

915 920 925

<210> 115
<211> 2877
<212> DNA
<213> Chimpanzee Adenovirus- ChAd 63 Hexon

<400> 115
atgtatgtcc gccgaccaga aggaggaaga ggcgcgtcgc cgagttgcaa gatggccacc 60
ccatcgatgc tgccccagtg ggcgtacatg cacatcgccg gacaggacgc ttcggagtac 120
ctgagtccgg gtctggtgca gttcgcccgc gccacagaca cctacttcag tctggggaac 180
aagtttagga accccacggt ggcgcccacg cacgatgtga ccaccgaccg cagccagcgg 240
ctgacgctgc gcttcgtgcc cgtggaccgc gaggacaaca cctactcgta caaagtgcgc 300
tacacgctgg ccgtgggcga caaccgcgtg ctggacatgg ccagcaccta ctttgacatc 360
cgcggcgtgc tggatcgggg ccccagcttc aaaccctact ccggcaccgc ctacaacagc 420
ctagctccca agggagcgcc caacacctca cagtggaagg attccgacag caaaatgcat 480
acttttggag ttgctgccat gcccggtgtt gttggtaaaa aaatagaagc cgatggtctg 540
cctattggaa tagattcatc ctctggaact gacaccataa tttatgctga taaaactttc 600
caaccagagc cacaggttgg aagtgacagt tgggtcgaca ccaatggtgc agaggaaaaa 660
tatggaggta gagctcttaa ggacactaca aacatgaagc cctgctacgg ttcttttgcc 720
aggcctacca acaaagaagg tggacaggct aacataaaag attctgaaac tgccagcact 780
actcctaact atgatataga tttggcattc tttgacagca aaaatattgc agctaactac 840
gatccagata ttgtaatgta cacagaaaat gttgagttgc aaactccaga tactcatatt 900
gtgtttaagc caggaacttc agatgaaagt tcagaagcca atttgggcca gcaggccatg 960
cccaacagac ccaactacat cgggttcaga gacaacttta tcgggctcat gtactacaac 1020
agcactggca atatgggtgt actggctggt caggcctccc agctaaatgc tgtggtggac 1080
ttgcaggaca gaaacaccga actgtcctac cagctcttgc ttgactctct gggtgacaga 1140
accaggtatt tcagtatgtg gaatcaggcg gtggacagct atgaccccga tgtgcgcatt 1200
attgaaaatc acggtgtgga ggatgaactc cccaattatt gcttcccttt gaatggtgta 1260
ggctttacag atacttacca gggtgttaaa gttaagacag atacagccgc tactggtacc 1320
aatggaacgc agtgggacaa agatgatacc acagtcagca ctgccaatga gatccactca 1380
ggcaatcctt tcgccatgga gatcaacatc caggccaacc tgtggcggaa cttcctctac 1440
gcgaacgtgg cgctgtacct gcccgactcc tacaagtaca cgccggccaa catcacgctg 1500
ccgaccaaca ccaacaccta cgattacatg aacggccgcg tggtggcgcc ctcgctggtg 1560
gacgcctaca tcaacatcgg ggcgcgctgg tcgctggacc ccatggacaa cgtcaacccc 1620
ttcaaccacc accgcaacgc gggcctgcgc taccgctcca tgctcctggg caacgggcgc 1680
tacgtgccct tccacatcca ggtgccccaa aagtttttcg ccatcaagag cctcctgctc 1740
ctgcccgggt cctacaccta cgagtggaac ttccgcaagg acgtcaacat gatcctgcag 1800
agctccctcg gcaacgacct gcgcacggac ggggcctcca tcgccttcac cagcatcaac 1860
ctctacgcca ccttcttccc catggcgcac aacaccgcct ccacgctcga ggccatgctg 1920
cgcaacgaca ccaacgacca gtccttcaac gactacctct cggcggccaa catgctctac 1980
cccatcccgg ccaacgccac caacgtgccc atctccatcc cctcgcgcaa ctgggccgcc 2040
ttccgcggat ggtccttcac gcgcctcaag acccgcgaga cgccctcgct cggctccggg 2100
ttcgacccct acttcgtcta ctcgggctcc atcccctacc tcgacggcac cttctacctc 2160
aaccacacct tcaagaaggt ctccatcacc ttcgactcct ccgtcagctg gcccggcaac 2220
gaccgcctcc tgacgcccaa cgagttcgaa atcaagcgca ccgtcgacgg agagggatac 2280
aacgtggccc agtgcaacat gaccaaggac tggttcctgg tccagatgct ggcccactac 2340
aacatcggct accagggctt ctacgtgccc gagggctaca aggaccgcat gtactccttc 2400
ttccgcaact tccagcccat gagccgccag gtcgtggacg aggtcaacta caaggactac 2460
caggccgtca ccctggccta ccagcacaac aactcgggct tcgtcggcta cctcgcgccc 2520
accatgcgcc agggccagcc ctaccccgcc aactacccct acccgctcat cggcaagagc 2580
gccgtcgcca gcgtcaccca gaaaaagttc ctctgcgacc gggtcatgtg gcgcatcccc 2640
ttctccagca acttcatgtc catgggcgcg ctcaccgacc tcggccagaa catgctctac 2700
gccaactccg cccacgcgct agacatgaat ttcgaagtcg accccatgga tgagtccacc 2760

cttctctatg ttgtcttcga agtcttcgac gtcgtccgag tgcaccagcc ccaccgcggc 2820
gtcatcgagg ccgtctacct gcgcacgccc ttctcggccg gcaacgccac cacctaa 2877

<210> 116
<211> 941
<212> PRT
<213> Chimpanzee Adenovirus- ChAd 63 Hexon

<400> 116
Met Ala Thr Pro Ser Met Leu Pro Gln Trp Ala Tyr Met His Ile Ala
1 5 10 15
Gly Gln Asp Ala Ser Glu Tyr Leu Ser Pro Gly Leu Val Gln Phe Ala
20 25 30
Arg Ala Thr Asp Thr Tyr Phe Ser Leu Gly Asn Lys Phe Arg Asn Pro
35 40 45
Thr Val Ala Pro Thr His Asp Val Thr Thr Asp Arg Ser Gln Arg Leu
50 55 60
Thr Leu Arg Phe Val Pro Val Asp Arg Glu Asp Asn Thr Tyr Ser Tyr
65 70 75 80
Lys Val Arg Tyr Thr Leu Ala Val Gly Asp Asn Arg Val Leu Asp Met
85 90 95
Ala Ser Thr Tyr Phe Asp Ile Arg Gly Val Leu Asp Arg Gly Pro Ser
100 105 110
Phe Lys Pro Tyr Ser Gly Thr Ala Tyr Asn Ser Leu Ala Pro Lys Gly
115 120 125
Ala Pro Asn Thr Ser Gln Trp Lys Asp Ser Asp Ser Lys Met His Thr
130 135 140
Phe Gly Val Ala Ala Met Pro Gly Val Val Gly Lys Lys Ile Glu Ala
145 150 155 160
Asp Gly Leu Pro Ile Gly Ile Asp Ser Ser Ser Gly Thr Asp Thr Ile
165 170 175
Ile Tyr Ala Asp Lys Thr Phe Gln Pro Glu Pro Gln Val Gly Ser Asp
180 185 190
Ser Trp Val Asp Thr Asn Gly Ala Glu Glu Lys Tyr Gly Gly Arg Ala
195 200 205
Leu Lys Asp Thr Thr Asn Met Lys Pro Cys Tyr Gly Ser Phe Ala Arg
210 215 220
Pro Thr Asn Lys Glu Gly Gly Gln Ala Asn Ile Lys Asp Ser Glu Thr
225 230 235 240
Ala Ser Thr Thr Pro Asn Tyr Asp Ile Asp Leu Ala Phe Phe Asp Ser
245 250 255
Lys Asn Ile Ala Ala Asn Tyr Asp Pro Asp Ile Val Met Tyr Thr Glu
260 265 270
Asn Val Glu Leu Gln Thr Pro Asp Thr His Ile Val Phe Lys Pro Gly
275 280 285
Thr Ser Asp Glu Ser Ser Glu Ala Asn Leu Gly Gln Gln Ala Met Pro
290 295 300
Asn Arg Pro Asn Tyr Ile Gly Phe Arg Asp Asn Phe Ile Gly Leu Met
305 310 315 320
Tyr Tyr Asn Ser Thr Gly Asn Met Gly Val Leu Ala Gly Gln Ala Ser
325 330 335
Gln Leu Asn Ala Val Val Asp Leu Gln Asp Arg Asn Thr Glu Leu Ser
340 345 350
Tyr Gln Leu Leu Leu Asp Ser Leu Gly Asp Arg Thr Arg Tyr Phe Ser
355 360 365

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Met Trp Asn Gln Ala Val Asp Ser Tyr Asp Pro Asp Val Arg Ile Ile
    370                 375                 380
Glu Asn His Gly Val Glu Asp Glu Leu Pro Asn Tyr Cys Phe Pro Leu
385                 390                 395                 400
Asn Gly Val Gly Phe Thr Asp Thr Tyr Gln Gly Val Lys Val Lys Thr
                405                 410                 415
Asp Thr Ala Ala Thr Gly Thr Asn Gly Thr Gln Trp Asp Lys Asp Asp
            420                 425                 430
Thr Thr Val Ser Thr Ala Asn Glu Ile His Ser Gly Asn Pro Phe Ala
        435                 440                 445
Met Glu Ile Asn Ile Gln Ala Asn Leu Trp Arg Asn Phe Leu Tyr Ala
    450                 455                 460
Asn Val Ala Leu Tyr Leu Pro Asp Ser Tyr Lys Tyr Thr Pro Ala Asn
465                 470                 475                 480
Ile Thr Leu Pro Thr Asn Thr Asn Thr Tyr Asp Tyr Met Asn Gly Arg
                485                 490                 495
Val Val Ala Pro Ser Leu Val Asp Ala Tyr Ile Asn Ile Gly Ala Arg
            500                 505                 510
Trp Ser Leu Asp Pro Met Asp Asn Val Asn Pro Phe Asn His His Arg
        515                 520                 525
Asn Ala Gly Leu Arg Tyr Arg Ser Met Leu Leu Gly Asn Gly Arg Tyr
    530                 535                 540
Val Pro Phe His Ile Gln Val Pro Gln Lys Phe Phe Ala Ile Lys Ser
545                 550                 555                 560
Leu Leu Leu Leu Pro Gly Ser Tyr Thr Tyr Glu Trp Asn Phe Arg Lys
                565                 570                 575
Asp Val Asn Met Ile Leu Gln Ser Ser Leu Gly Asn Asp Leu Arg Thr
            580                 585                 590
Asp Gly Ala Ser Ile Ala Phe Thr Ser Ile Asn Leu Tyr Ala Thr Phe
        595                 600                 605
Phe Pro Met Ala His Asn Thr Ala Ser Thr Leu Glu Ala Met Leu Arg
    610                 615                 620
Asn Asp Thr Asn Asp Gln Ser Phe Asn Asp Tyr Leu Ser Ala Ala Asn
625                 630                 635                 640
Met Leu Tyr Pro Ile Pro Ala Asn Ala Thr Asn Val Pro Ile Ser Ile
                645                 650                 655
Pro Ser Arg Asn Trp Ala Ala Phe Arg Gly Trp Ser Phe Thr Arg Leu
            660                 665                 670
Lys Thr Arg Glu Thr Pro Ser Leu Gly Ser Gly Phe Asp Pro Tyr Phe
        675                 680                 685
Val Tyr Ser Gly Ser Ile Pro Tyr Leu Asp Gly Thr Phe Tyr Leu Asn
    690                 695                 700
His Thr Phe Lys Lys Val Ser Ile Thr Phe Asp Ser Ser Val Ser Trp
705                 710                 715                 720
Pro Gly Asn Asp Arg Leu Leu Thr Pro Asn Glu Phe Glu Ile Lys Arg
                725                 730                 735
Thr Val Asp Gly Glu Gly Tyr Asn Val Ala Gln Cys Asn Met Thr Lys
            740                 745                 750
Asp Trp Phe Leu Val Gln Met Leu Ala His Tyr Asn Ile Gly Tyr Gln
        755                 760                 765
Gly Phe Tyr Val Pro Glu Gly Tyr Lys Asp Arg Met Tyr Ser Phe Phe
    770                 775                 780
Arg Asn Phe Gln Pro Met Ser Arg Gln Val Val Asp Glu Val Asn Tyr
785                 790                 795                 800
Lys Asp Tyr Gln Ala Val Thr Leu Ala Tyr Gln His Asn Asn Ser Gly
```

```
                805                 810                 815
Phe Val Gly Tyr Leu Ala Pro Thr Met Arg Gln Gly Gln Pro Tyr Pro
            820                 825                 830
Ala Asn Tyr Pro Tyr Pro Leu Ile Gly Lys Ser Ala Val Ala Ser Val
        835                 840                 845
Thr Gln Lys Lys Phe Leu Cys Asp Arg Val Met Trp Arg Ile Pro Phe
    850                 855                 860
Ser Ser Asn Phe Met Ser Met Gly Ala Leu Thr Asp Leu Gly Gln Asn
865                 870                 875                 880
Met Leu Tyr Ala Asn Ser Ala His Ala Leu Asp Met Asn Phe Glu Val
                885                 890                 895
Asp Pro Met Asp Glu Ser Thr Leu Leu Tyr Val Val Phe Glu Val Phe
            900                 905                 910
Asp Val Val Arg Val His Gln Pro His Arg Gly Val Ile Glu Ala Val
        915                 920                 925
Tyr Leu Arg Thr Pro Phe Ser Ala Gly Asn Ala Thr Thr
    930                 935                 940
```

<210> 117
<211> 2811
<212> DNA
<213> Chimpanzee Adenovirus- ChAd 82 Hexon

<400> 117

```
atggccaccc catcgatgct gccccagtgg gcgtacatgc acatcgccgg acaggacgct 60
tcggagtacc tgagtccggg tctggtgcag ttcgcccgcg ccacagacac ctacttcagt 120
ctggggaaca agtttaggaa ccccacggtg gcgcccacgc acgatgtgac caccgaccgc 180
agccagcggc tgacgctgcg cttcgtgccc gtggaccgcg aggacaacac ctactcgtac 240
aaagtgcgct acacgctggc cgtgggcgac aaccgcgtgc tggacatggc cagcacttac 300
tttgacatcc gcggcgtgct ggaccggggc cctagcttca aaccctactc cggcaccgcc 360
tacaacagcc tggctcccaa gggagcgccc aattccagcc agtgggagca aaatgaaaac 420
aatggtcaag gtcaagctaa gacacacacc tatggtgttg ctgctatggg cggacttgat 480
attacaaaag agggtcttaa aattgtaact gatgctagta aggaagatga caatgaaatt 540
tatgcagata aaacatatca gcccgagcct caaataggag aggaaaattg gcaagacact 600
aaaaactttt atggaggcag agctcttaaa aaagatacca agatgaagcc atgctatggc 660
tcatttgcca gacctaccaa tgtgaaggga gggcaagcca aagtgaaaac agaagaaaat 720
gttcagtcat ttgacataga tctggctttc tttgatattc caagcaccgg cacaggggc 780
aatggtacaa atgtaaatga taagccagac atggttatgt acactgaaaa tgtgaatctg 840
gagacgccag atactcatat tgtgtacaaa cctggaactt cagatgacag ctctgaagcc 900
aacttgtgcc agcaggccat gccaaacaga cccaactaca ttggtttcag agacaacttt 960
attgggctca tgtattacaa cagtactggc aatatggggg tgctggctgg tcaggcctcc 1020
cagctgaatg ctgtggttga cttgcaagac agaaacaccg agctgtcata ccagctcttg 1080
cttgactctc tgggtgacag aacccggtat ttcagcatgt ggaaccaggc ggtggacagt 1140
tatgaccctg atgtgcgcat tattgaaaac catggtgtgg aggatgaatt gccaaactat 1200
tgcttccct tggatggagc tggcactaat gctgtatacc ggggtgttaa agcaaaagat 1260
aacggaaact gggaacaaga cacaggcgtt tcaagtatta accagatatg caaggggaac 1320
atctatgcca tggaaatcaa cattcaagcc aacctgtgga gaagtttcct ttactcgaac 1380
gtggccctgt acctgcccga ctcttacaag tacacgccgg ccaacatcac cctgcccacc 1440
aacaccaaca cctacgatta catgaacggt cgggtggtgc ctccctcgct ggtggacgcc 1500
tacatcaaca tcggggcgcg ctggtcgctg gaccccatgg acaacgtcaa tcccttcaac 1560
caccaccgca acgcgggcct gcgctaccgc tccatgctcc tgggcaacgg gcgctacgtg 1620
cccttccaca tccaggtgcc ccagaaattt ttcgccatca agagcctcct gctcctgccc 1680
gggtcctaca cctacgagtg gaacttccgc aaggacgtca acatgatcct gcagagctcc 1740
ctcggcaacg acctgcgcac ggacggggcc tccatctcct tcaccagcat caacctctac 1800
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gccaccttct tccccatggc gcacaacacg gcctccacgc tcgaggccat gctgcgcaac 1860
gacaccaacg accagtcctt caacgactac ctctcggcgg ccaacatgct ctaccccatc 1920
ccggccaacg ccaccaacgt gcccatctcc atcccctcgc gcaactgggc cgccttccgc 1980
ggctggtcct tcacgcgtct caagaccaag gagacgccct cgctgggctc cgggttcgac 2040
ccctacttcg tctactcggg ctccatcccc tacctcgacg gcaccttcta cctcaaccac 2100
accttcaaga aggtctccat caccttcgac tcctccgtca gctggcccgg caacgaccgg 2160
ctcctgacgc ccaacgagtt cgaaatcaag cgcaccgtcg acggcgaggg ctacaacgtg 2220
gcccagtgca acatgaccaa ggactggttc ctggtccaga tgctggccca ctacaacatc 2280
ggctaccagg gcttctacgt gcccgagggc tacaaggacc gcatgtactc cttcttccgc 2340
aacttccagc ccatgagccg ccaggtggtg gacgaggtca actacaagga ctaccaggcc 2400
gtcaccctgg cctaccagca caacaactcg ggcttcgtcg gctacctcgc gcccaccatg 2460
cgccaggggc agccctaccc cgccaactac ccgtacccgc tcatcggcaa gagcgccgtc 2520
accagcgtca cccagaaaaa gttcctctgc gacagggtca tgtggcgcat ccccttctcc 2580
agcaacttca tgtccatggg cgcgctcacc gacctcggcc agaacatgct ctatgccaac 2640
tccgcccacg cgctagacat gaatttcgaa gtcgacccca tggatgagtc cacccttctc 2700
tatgttgtct tcgaagtctt cgacgtcgtc cgagtgcacc agccccaccg cggcgtcatc 2760
gaggccgtct acctgcgcac acccttctcg gccggtaacg ccaccaccta a          2811

<210> 118
<211> 936
<212> PRT
<213> Chimpanzee Adenovirus- ChAd 82 Hexon

<400> 118
Met Ala Thr Pro Ser Met Leu Pro Gln Trp Ala Tyr Met His Ile Ala
 1               5                  10                  15
Gly Gln Asp Ala Ser Glu Tyr Leu Ser Pro Gly Leu Val Gln Phe Ala
            20                  25                  30
Arg Ala Thr Asp Thr Tyr Phe Ser Leu Gly Asn Lys Phe Arg Asn Pro
        35                  40                  45
Thr Val Ala Pro Thr His Asp Val Thr Thr Asp Arg Ser Gln Arg Leu
    50                  55                  60
Thr Leu Arg Phe Val Pro Val Asp Arg Glu Asp Asn Thr Tyr Ser Tyr
65                  70                  75                  80
Lys Val Arg Tyr Thr Leu Ala Val Gly Asp Asn Arg Val Leu Asp Met
                85                  90                  95
Ala Ser Thr Tyr Phe Asp Ile Arg Gly Val Leu Asp Arg Gly Pro Ser
            100                 105                 110
Phe Lys Pro Tyr Ser Gly Thr Ala Tyr Asn Ser Leu Ala Pro Lys Gly
        115                 120                 125
Ala Pro Asn Ser Ser Gln Trp Glu Gln Asn Glu Asn Asn Gly Gln Gly
    130                 135                 140
Gln Ala Lys Thr His Thr Tyr Gly Val Ala Ala Met Gly Gly Leu Asp
145                 150                 155                 160
Ile Thr Lys Glu Gly Leu Lys Ile Val Thr Asp Ala Ser Lys Glu Asp
                165                 170                 175
Asp Asn Glu Ile Tyr Ala Asp Lys Thr Tyr Gln Pro Glu Pro Gln Ile
            180                 185                 190
Gly Glu Glu Asn Trp Gln Asp Thr Lys Asn Phe Tyr Gly Gly Arg Ala
        195                 200                 205
Leu Lys Lys Asp Thr Lys Met Lys Pro Cys Tyr Gly Ser Phe Ala Arg
    210                 215                 220
Pro Thr Asn Val Lys Gly Gly Gln Ala Lys Val Lys Thr Glu Glu Asn
225                 230                 235                 240
Val Gln Ser Phe Asp Ile Asp Leu Ala Phe Phe Asp Ile Pro Ser Thr
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                245                 250                 255
Gly Thr Gly Gly Asn Gly Thr Asn Val Asn Asp Lys Pro Asp Met Val
            260                 265                 270
Met Tyr Thr Glu Asn Val Asn Leu Glu Thr Pro Asp Thr His Ile Val
        275                 280                 285
Tyr Lys Pro Gly Thr Ser Asp Asp Ser Ser Glu Ala Asn Leu Cys Gln
    290                 295                 300
Gln Ala Met Pro Asn Arg Pro Asn Tyr Ile Gly Phe Arg Asp Asn Phe
305                 310                 315                 320
Ile Gly Leu Met Tyr Tyr Asn Ser Thr Gly Asn Met Gly Val Leu Ala
                325                 330                 335
Gly Gln Ala Ser Gln Leu Asn Ala Val Val Asp Leu Gln Asp Arg Asn
            340                 345                 350
Thr Glu Leu Ser Tyr Gln Leu Leu Leu Asp Ser Leu Gly Asp Arg Thr
        355                 360                 365
Arg Tyr Phe Ser Met Trp Asn Gln Ala Val Asp Ser Tyr Asp Pro Asp
    370                 375                 380
Val Arg Ile Ile Glu Asn His Gly Val Glu Asp Glu Leu Pro Asn Tyr
385                 390                 395                 400
Cys Phe Pro Leu Asp Gly Ala Gly Thr Asn Ala Val Tyr Arg Gly Val
                405                 410                 415
Lys Ala Lys Asp Asn Gly Asn Trp Glu Gln Asp Thr Gly Val Ser Ser
            420                 425                 430
Ile Asn Gln Ile Cys Lys Gly Asn Ile Tyr Ala Met Glu Ile Asn Ile
        435                 440                 445
Gln Ala Asn Leu Trp Arg Ser Phe Leu Tyr Ser Asn Val Ala Leu Tyr
    450                 455                 460
Leu Pro Asp Ser Tyr Lys Tyr Thr Pro Ala Asn Ile Thr Leu Pro Thr
465                 470                 475                 480
Asn Thr Asn Thr Tyr Asp Tyr Met Asn Gly Arg Val Val Pro Pro Ser
                485                 490                 495
Leu Val Asp Ala Tyr Ile Asn Ile Gly Ala Arg Trp Ser Leu Asp Pro
            500                 505                 510
Met Asp Asn Val Asn Pro Phe Asn His His Arg Asn Ala Gly Leu Arg
        515                 520                 525
Tyr Arg Ser Met Leu Leu Gly Asn Gly Arg Tyr Val Pro Phe His Ile
    530                 535                 540
Gln Val Pro Gln Lys Phe Phe Ala Ile Lys Ser Leu Leu Leu Leu Pro
545                 550                 555                 560
Gly Ser Tyr Thr Tyr Glu Trp Asn Phe Arg Lys Asp Val Asn Met Ile
                565                 570                 575
Leu Gln Ser Ser Leu Gly Asn Asp Leu Arg Thr Asp Gly Ala Ser Ile
            580                 585                 590
Ser Phe Thr Ser Ile Asn Leu Tyr Ala Thr Phe Phe Pro Met Ala His
        595                 600                 605
Asn Thr Ala Ser Thr Leu Glu Ala Met Leu Arg Asn Asp Thr Asn Asp
    610                 615                 620
Gln Ser Phe Asn Asp Tyr Leu Ser Ala Ala Asn Met Leu Tyr Pro Ile
625                 630                 635                 640
Pro Ala Asn Ala Thr Asn Val Pro Ile Ser Ile Pro Ser Arg Asn Trp
                645                 650                 655
Ala Ala Phe Arg Gly Trp Ser Phe Thr Arg Leu Lys Thr Lys Glu Thr
            660                 665                 670
Pro Ser Leu Gly Ser Gly Phe Asp Pro Tyr Phe Val Tyr Ser Gly Ser
        675                 680                 685
```

```
Ile Pro Tyr Leu Asp Gly Thr Phe Tyr Leu Asn His Thr Phe Lys Lys
    690                 695                 700
Val Ser Ile Thr Phe Asp Ser Ser Val Ser Trp Pro Gly Asn Asp Arg
705                 710                 715                 720
Leu Leu Thr Pro Asn Glu Phe Glu Ile Lys Arg Thr Val Asp Gly Glu
                725                 730                 735
Gly Tyr Asn Val Ala Gln Cys Asn Met Thr Lys Asp Trp Phe Leu Val
            740                 745                 750
Gln Met Leu Ala His Tyr Asn Ile Gly Tyr Gln Gly Phe Tyr Val Pro
        755                 760                 765
Glu Gly Tyr Lys Asp Arg Met Tyr Ser Phe Phe Arg Asn Phe Gln Pro
    770                 775                 780
Met Ser Arg Gln Val Val Asp Glu Val Asn Tyr Lys Asp Tyr Gln Ala
785                 790                 795                 800
Val Thr Leu Ala Tyr Gln His Asn Asn Ser Gly Phe Val Gly Tyr Leu
                805                 810                 815
Ala Pro Thr Met Arg Gln Gly Gln Pro Tyr Pro Ala Asn Tyr Pro Tyr
            820                 825                 830
Pro Leu Ile Gly Lys Ser Ala Val Thr Ser Val Thr Gln Lys Lys Phe
        835                 840                 845
Leu Cys Asp Arg Val Met Trp Arg Ile Pro Phe Ser Ser Asn Phe Met
    850                 855                 860
Ser Met Gly Ala Leu Thr Asp Leu Gly Gln Asn Met Leu Tyr Ala Asn
865                 870                 875                 880
Ser Ala His Ala Leu Asp Met Asn Phe Glu Val Asp Pro Met Asp Glu
                885                 890                 895
Ser Thr Leu Leu Tyr Val Val Phe Glu Val Phe Asp Val Val Arg Val
            900                 905                 910
His Gln Pro His Arg Gly Val Ile Glu Ala Val Tyr Leu Arg Thr Pro
        915                 920                 925
Phe Ser Ala Gly Asn Ala Thr Thr
    930                 935
```

<210> 119
<211> 933
<212> PRT
<213> Chimpanzee Adenovirus- CV23 Pan5 Hexon

<400> 119

```
Met Ala Thr Pro Ser Met Leu Pro Gln Trp Ala Tyr Met His Ile Ala
 1                5                  10                  15
Gly Gln Asp Ala Ser Glu Tyr Leu Ser Pro Gly Leu Val Gln Phe Ala
            20                  25                  30
Arg Ala Thr Asp Thr Tyr Phe Ser Leu Gly Asn Lys Phe Arg Asn Pro
        35                  40                  45
Thr Val Ala Pro Thr His Asp Val Thr Thr Asp Arg Ser Gln Arg Leu
    50                  55                  60
Thr Leu Arg Phe Val Pro Val Asp Arg Glu Asp Asn Thr Tyr Ser Tyr
65                  70                  75                  80
Lys Val Arg Tyr Thr Leu Ala Val Gly Asp Asn Arg Val Leu Asp Met
                85                  90                  95
Ala Ser Thr Tyr Phe Asp Ile Arg Gly Val Leu Asp Arg Gly Pro Ser
            100                 105                 110
Phe Lys Pro Tyr Ser Gly Thr Ala Tyr Asn Ser Leu Ala Pro Lys Gly
```

```
        115                 120                 125
Ala Pro Asn Thr Cys Gln Trp Thr Tyr Lys Ala Asp Gly Asp Thr Gly
    130                 135                 140
Thr Glu Lys Thr Tyr Thr Tyr Gly Asn Ala Pro Val Gln Gly Ile Ser
145                 150                 155                 160
Ile Thr Lys Asp Gly Ile Gln Leu Gly Thr Asp Thr Asp Asp Gln Pro
                165                 170                 175
Ile Tyr Ala Asp Lys Thr Tyr Gln Pro Glu Pro Gln Val Gly Asp Ala
            180                 185                 190
Glu Trp His Asp Ile Thr Gly Thr Asp Glu Lys Tyr Gly Gly Arg Ala
        195                 200                 205
Leu Lys Pro Asp Thr Lys Met Lys Pro Cys Tyr Gly Ser Phe Ala Lys
    210                 215                 220
Pro Thr Asn Lys Glu Gly Gly Gln Ala Asn Val Lys Thr Glu Thr Gly
225                 230                 235                 240
Gly Thr Lys Glu Tyr Asp Ile Asp Met Ala Phe Phe Asp Asn Arg Ser
                245                 250                 255
Ala Ala Ala Ala Gly Leu Ala Pro Glu Ile Val Leu Tyr Thr Glu Asn
            260                 265                 270
Val Asp Leu Glu Thr Pro Asp Thr His Ile Val Tyr Lys Ala Gly Thr
        275                 280                 285
Asp Asp Ser Ser Ser Ser Ile Asn Leu Gly Gln Gln Ser Met Pro Asn
    290                 295                 300
Arg Pro Asn Tyr Ile Gly Phe Arg Asp Asn Phe Ile Gly Leu Met Tyr
305                 310                 315                 320
Tyr Asn Ser Thr Gly Asn Met Gly Val Leu Ala Gly Gln Ala Ser Gln
                325                 330                 335
Leu Asn Ala Val Val Asp Leu Gln Asp Arg Asn Thr Glu Leu Ser Tyr
            340                 345                 350
Gln Leu Leu Leu Asp Ser Leu Gly Asp Arg Thr Arg Tyr Phe Ser Met
        355                 360                 365
Trp Asn Gln Ala Val Asp Ser Tyr Asp Pro Asp Val Arg Ile Ile Glu
    370                 375                 380
Asn His Gly Val Glu Asp Glu Leu Pro Asn Tyr Cys Phe Pro Leu Asp
385                 390                 395                 400
Ala Val Gly Arg Thr Asp Thr Tyr Gln Gly Ile Lys Ala Asn Gly Ala
                405                 410                 415
Asp Gln Thr Thr Trp Thr Lys Asp Asp Thr Val Asn Asp Ala Asn Glu
            420                 425                 430
Leu Gly Lys Gly Asn Pro Phe Ala Met Glu Ile Asn Ile Gln Ala Asn
        435                 440                 445
Leu Trp Arg Asn Phe Leu Tyr Ala Asn Val Ala Leu Tyr Leu Pro Asp
    450                 455                 460
Ser Tyr Lys Tyr Thr Pro Ala Asn Ile Thr Leu Pro Thr Asn Thr Asn
465                 470                 475                 480
Thr Tyr Asp Tyr Met Asn Gly Arg Val Val Ala Pro Ser Leu Val Asp
                485                 490                 495
Ala Tyr Ile Asn Ile Gly Ala Arg Trp Ser Leu Asp Pro Met Asp Asn
            500                 505                 510
Val Asn Pro Phe Asn His His Arg Asn Ala Gly Leu Arg Tyr Arg Ser
        515                 520                 525
Met Leu Leu Gly Asn Gly Arg Tyr Val Pro Phe His Ile Gln Val Pro
    530                 535                 540
Gln Lys Phe Phe Ala Ile Lys Ser Leu Leu Leu Leu Pro Gly Ser Tyr
545                 550                 555                 560
```

```
Thr Tyr Glu Trp Asn Phe Arg Lys Asp Val Asn Met Ile Leu Gln Ser
                565                 570                 575
Ser Leu Gly Asn Asp Leu Arg Thr Asp Gly Ala Ser Ile Ala Phe Thr
            580                 585                 590
Ser Ile Asn Leu Tyr Ala Thr Phe Phe Pro Met Ala His Asn Thr Ala
        595                 600                 605
Ser Thr Leu Glu Ala Met Leu Arg Asn Asp Thr Asn Asp Gln Ser Phe
    610                 615                 620
Asn Asp Tyr Leu Ser Ala Ala Asn Met Leu Tyr Pro Ile Pro Ala Asn
625                 630                 635                 640
Ala Thr Asn Val Pro Ile Ser Ile Pro Ser Arg Asn Trp Ala Ala Phe
                645                 650                 655
Arg Gly Trp Ser Phe Thr Arg Leu Lys Thr Arg Glu Thr Pro Ser Leu
            660                 665                 670
Gly Ser Gly Phe Asp Pro Tyr Phe Val Tyr Ser Gly Ser Ile Pro Tyr
        675                 680                 685
Leu Asp Gly Thr Phe Tyr Leu Asn His Thr Phe Lys Lys Val Ser Ile
    690                 695                 700
Thr Phe Asp Ser Ser Val Ser Trp Pro Gly Asn Asp Arg Leu Leu Thr
705                 710                 715                 720
Pro Asn Glu Phe Glu Ile Lys Arg Thr Val Asp Gly Glu Gly Tyr Asn
                725                 730                 735
Val Ala Gln Cys Asn Met Thr Lys Asp Trp Phe Leu Val Gln Met Leu
            740                 745                 750
Ala His Tyr Asn Ile Gly Tyr Gln Gly Phe Tyr Val Pro Glu Gly Tyr
        755                 760                 765
Lys Asp Arg Met Tyr Ser Phe Phe Arg Asn Phe Gln Pro Met Ser Arg
    770                 775                 780
Gln Val Val Asp Glu Val Asn Tyr Lys Asp Tyr Gln Ala Val Thr Leu
785                 790                 795                 800
Ala Tyr Gln His Asn Asn Ser Gly Phe Val Gly Tyr Leu Ala Pro Thr
                805                 810                 815
Met Arg Gln Gly Gln Pro Tyr Pro Ala Asn Tyr Pro Tyr Pro Leu Ile
            820                 825                 830
Gly Lys Ser Ala Val Ala Ser Val Thr Gln Lys Lys Phe Leu Cys Asp
        835                 840                 845
Arg Val Met Trp Arg Ile Pro Phe Ser Ser Asn Phe Met Ser Met Gly
    850                 855                 860
Ala Leu Thr Asp Leu Gly Gln Asn Met Leu Tyr Ala Asn Ser Ala His
865                 870                 875                 880
Ala Leu Asp Met Asn Phe Glu Val Asp Pro Met Asp Glu Ser Thr Leu
                885                 890                 895
Leu Tyr Val Val Phe Glu Val Phe Asp Val Val Arg Val His Gln Pro
            900                 905                 910
His Arg Gly Val Ile Glu Ala Val Tyr Leu Arg Thr Pro Phe Ser Ala
        915                 920                 925
Gly Asn Ala Thr Thr
    930
```

<210> 120
<211> 942
<212> PRT
<213> Chimpanzee Adenovirus- CV32 Pan6 Hexon

<400> 120

```
Met Ala Thr Pro Ser Met Leu Pro Gln Trp Ala Tyr Met His Ile Ala
 1               5                  10                  15
Gly Gln Asp Ala Ser Glu Tyr Leu Ser Pro Gly Leu Val Gln Phe Ala
            20                  25                  30
Arg Ala Thr Asp Thr Tyr Phe Ser Leu Gly Asn Lys Phe Arg Asn Pro
        35                  40                  45
Thr Val Ala Pro Thr His Asn Val Thr Thr Asp Arg Ser Gln Arg Leu
    50                  55                  60
Thr Val Arg Phe Val Pro Val Asp Arg Glu Asp Asn Thr Tyr Ser Tyr
65                  70                  75                  80
Lys Val Arg Tyr Thr Leu Ala Val Gly Asp Asn Arg Val Leu Asp Met
                85                  90                  95
Ala Ser Thr Tyr Phe Asp Ile Arg Gly Val Leu Asp Arg Gly Pro Ser
            100                 105                 110
Phe Lys Pro Tyr Ser Gly Thr Ala Tyr Asn Ser Leu Ala Pro Lys Gly
        115                 120                 125
Ala Pro Asn Ser Ser Gln Trp Glu Gln Ala Lys Thr Gly Asn Gly Gly
    130                 135                 140
Thr Met Glu Thr His Thr Tyr Gly Val Ala Pro Met Gly Gly Glu Asn
145                 150                 155                 160
Ile Thr Lys Asp Gly Leu Gln Ile Gly Thr Asp Val Thr Ala Asn Gln
                165                 170                 175
Asn Lys Pro Ile Tyr Ala Asp Lys Thr Phe Gln Pro Glu Pro Gln Val
            180                 185                 190
Gly Glu Glu Asn Trp Gln Glu Thr Glu Asn Phe Tyr Gly Gly Arg Ala
        195                 200                 205
Leu Lys Lys Asp Thr Asn Met Lys Pro Cys Tyr Gly Ser Tyr Ala Arg
    210                 215                 220
Pro Thr Asn Glu Lys Gly Gly Gln Ala Lys Leu Lys Val Gly Asp Asp
225                 230                 235                 240
Gly Val Pro Thr Lys Glu Phe Asp Ile Asp Leu Ala Phe Phe Asp Thr
                245                 250                 255
Pro Gly Gly Thr Val Asn Gly Gln Asp Glu Tyr Lys Ala Asp Ile Val
            260                 265                 270
Met Tyr Thr Glu Asn Thr Tyr Leu Glu Thr Pro Asp Thr His Val Val
        275                 280                 285
Tyr Lys Pro Gly Lys Asp Asp Ala Ser Ser Glu Ile Asn Leu Val Gln
    290                 295                 300
Gln Ser Met Pro Asn Arg Pro Asn Tyr Ile Gly Phe Arg Asp Asn Phe
305                 310                 315                 320
Ile Gly Leu Met Tyr Tyr Asn Ser Thr Gly Asn Met Gly Val Leu Ala
                325                 330                 335
Gly Gln Ala Ser Gln Leu Asn Ala Val Val Asp Leu Gln Asp Arg Asn
            340                 345                 350
Thr Glu Leu Ser Tyr Gln Leu Leu Leu Asp Ser Leu Gly Asp Arg Thr
        355                 360                 365
Arg Tyr Phe Ser Met Trp Asn Gln Ala Val Asp Ser Tyr Asp Pro Asp
    370                 375                 380
Val Arg Ile Ile Glu Asn His Gly Val Glu Asp Glu Leu Pro Asn Tyr
385                 390                 395                 400
Cys Phe Pro Leu Asp Gly Ser Gly Thr Asn Ala Ala Tyr Gln Gly Val
                405                 410                 415
Lys Val Lys Asp Gly Gln Asp Gly Asp Val Glu Ser Glu Trp Glu Asn
            420                 425                 430
```

```
Asp Asp Thr Val Ala Ala Arg Asn Gln Leu Cys Lys Gly Asn Ile Phe
        435                 440                 445
Ala Met Glu Ile Asn Leu Gln Ala Asn Leu Trp Arg Ser Phe Leu Tyr
    450                 455                 460
Ser Asn Val Ala Leu Tyr Leu Pro Asp Ser Tyr Lys Tyr Thr Pro Thr
465                 470                 475                 480
Asn Val Thr Leu Pro Thr Asn Thr Asn Thr Tyr Asp Tyr Met Asn Gly
                485                 490                 495
Arg Val Thr Pro Pro Ser Leu Val Asp Ala Tyr Leu Asn Ile Gly Ala
            500                 505                 510
Arg Trp Ser Leu Asp Pro Met Asp Asn Val Asn Pro Phe Asn His His
        515                 520                 525
Arg Asn Ala Gly Leu Arg Tyr Arg Ser Met Leu Leu Gly Asn Gly Arg
    530                 535                 540
Tyr Val Pro Phe His Ile Gln Val Pro Gln Lys Phe Phe Ala Ile Lys
545                 550                 555                 560
Ser Leu Leu Leu Leu Pro Gly Ser Tyr Thr Tyr Glu Trp Asn Phe Arg
                565                 570                 575
Lys Asp Val Asn Met Ile Leu Gln Ser Ser Leu Gly Asn Asp Leu Arg
            580                 585                 590
Thr Asp Gly Ala Ser Ile Ala Phe Thr Ser Ile Asn Leu Tyr Ala Thr
        595                 600                 605
Phe Phe Pro Met Ala His Asn Thr Ala Ser Thr Leu Glu Ala Met Leu
    610                 615                 620
Arg Asn Asp Thr Asn Asp Gln Ser Phe Asn Asp Tyr Leu Ser Ala Ala
625                 630                 635                 640
Asn Met Leu Tyr Pro Ile Pro Ala Asn Ala Thr Asn Val Pro Ile Ser
                645                 650                 655
Ile Pro Ser Arg Asn Trp Ala Ala Phe Arg Gly Trp Ser Phe Thr Arg
            660                 665                 670
Leu Lys Thr Arg Glu Thr Pro Ser Leu Gly Ser Gly Phe Asp Pro Tyr
        675                 680                 685
Phe Val Tyr Ser Gly Ser Ile Pro Tyr Leu Asp Gly Thr Phe Tyr Leu
    690                 695                 700
Asn His Thr Phe Lys Lys Val Ser Ile Thr Phe Asp Ser Ser Val Ser
705                 710                 715                 720
Trp Pro Gly Asn Asp Arg Leu Leu Thr Pro Asn Glu Phe Glu Ile Lys
                725                 730                 735
Arg Thr Val Asp Gly Glu Gly Tyr Asn Val Ala Gln Cys Asn Met Thr
            740                 745                 750
Lys Asp Trp Phe Leu Val Gln Met Leu Ala His Tyr Asn Ile Gly Tyr
        755                 760                 765
Gln Gly Phe Tyr Val Pro Glu Gly Tyr Lys Asp Arg Met Tyr Ser Phe
    770                 775                 780
Phe Arg Asn Phe Gln Pro Met Ser Arg Gln Val Val Asp Glu Val Asn
785                 790                 795                 800
Tyr Lys Asp Tyr Gln Ala Val Thr Leu Ala Tyr Gln His Asn Asn Ser
                805                 810                 815
Gly Phe Val Gly Tyr Leu Ala Pro Thr Met Arg Gln Gly Gln Pro Tyr
            820                 825                 830
Pro Ala Asn Tyr Pro Tyr Pro Leu Ile Gly Lys Ser Ala Val Ala Ser
        835                 840                 845
Val Thr Gln Lys Lys Phe Leu Cys Asp Arg Val Met Trp Arg Ile Pro
    850                 855                 860
Phe Ser Ser Asn Phe Met Ser Met Gly Ala Leu Thr Asp Leu Gly Gln
```

```
865                 870                 875                 880
Asn Met Leu Tyr Ala Asn Ser Ala His Ala Leu Asp Met Asn Phe Glu
                885                 890                 895
Val Asp Pro Met Asp Glu Ser Thr Leu Leu Tyr Val Val Phe Glu Val
            900                 905                 910
Phe Asp Val Val Arg Val His Gln Pro His Arg Gly Val Ile Glu Ala
        915                 920                 925
Val Tyr Leu Arg Thr Pro Phe Ser Ala Gly Asn Ala Thr Thr
    930                 935                 940
```

<210> 121
<211> 932
<212> PRT
<213> Chimpanzee Adenovirus- CV33 Pan7 Hexon

<400> 121

```
Met Ala Thr Pro Ser Met Leu Pro Gln Trp Ala Tyr Met His Ile Ala
 1               5                  10                  15
Gly Gln Asp Ala Ser Glu Tyr Leu Ser Pro Gly Leu Val Gln Phe Ala
            20                  25                  30
Arg Ala Thr Asp Thr Tyr Phe Ser Leu Gly Asn Lys Phe Arg Asn Pro
        35                  40                  45
Thr Val Ala Pro Thr His Asp Val Thr Thr Asp Arg Ser Gln Arg Leu
    50                  55                  60
Thr Leu Arg Phe Val Pro Val Asp Arg Glu Asp Asn Thr Tyr Ser Tyr
65                  70                  75                  80
Lys Val Arg Tyr Thr Leu Ala Val Gly Asp Asn Arg Val Leu Asp Met
                85                  90                  95
Ala Ser Thr Tyr Phe Asp Ile Arg Gly Val Leu Asp Arg Gly Pro Ser
            100                 105                 110
Phe Lys Pro Tyr Ser Gly Thr Ala Tyr Asn Ser Leu Ala Pro Lys Gly
        115                 120                 125
Ala Pro Asn Thr Cys Gln Trp Thr Tyr Lys Ala Gly Asp Thr Asp Thr
    130                 135                 140
Glu Lys Thr Tyr Thr Tyr Gly Asn Ala Pro Val Gln Gly Ile Ser Ile
145                 150                 155                 160
Thr Lys Asp Gly Ile Gln Leu Gly Thr Asp Ser Asp Gly Gln Ala Ile
                165                 170                 175
Tyr Ala Asp Glu Thr Tyr Gln Pro Glu Pro Gln Val Gly Asp Ala Glu
            180                 185                 190
Trp His Asp Ile Thr Gly Thr Asp Glu Lys Tyr Gly Gly Arg Ala Leu
        195                 200                 205
Lys Pro Asp Thr Lys Met Lys Pro Cys Tyr Gly Ser Phe Ala Lys Pro
    210                 215                 220
Thr Asn Lys Glu Gly Gly Gln Ala Asn Val Lys Thr Glu Thr Gly Gly
225                 230                 235                 240
Thr Lys Glu Tyr Asp Ile Asp Met Ala Phe Phe Asp Asn Arg Ser Ala
                245                 250                 255
Ala Ala Ala Gly Leu Ala Pro Glu Ile Val Leu Tyr Thr Glu Asn Val
            260                 265                 270
Asp Leu Glu Thr Pro Asp Thr His Ile Val Tyr Lys Ala Gly Thr Asp
        275                 280                 285
Asp Ser Ser Ser Ser Ile Asn Leu Gly Gln Gln Ser Met Pro Asn Arg
    290                 295                 300
```

```
Pro Asn Tyr Ile Gly Phe Arg Asp Asn Phe Ile Gly Leu Met Tyr Tyr
305                 310                 315                 320
Asn Ser Thr Gly Asn Met Gly Val Leu Ala Gly Gln Ala Ser Gln Leu
                325                 330                 335
Asn Ala Val Val Asp Leu Gln Asp Arg Asn Thr Glu Leu Ser Tyr Gln
            340                 345                 350
Leu Leu Leu Asp Ser Leu Gly Asp Arg Thr Arg Tyr Phe Ser Met Trp
        355                 360                 365
Asn Gln Ala Val Asp Ser Tyr Asp Pro Asp Val Arg Ile Ile Glu Asn
    370                 375                 380
His Gly Val Glu Asp Glu Leu Pro Asn Tyr Cys Phe Pro Leu Asp Ala
385                 390                 395                 400
Val Gly Arg Thr Asp Thr Tyr Gln Gly Ile Lys Ala Asn Gly Asp Asn
                405                 410                 415
Gln Thr Thr Trp Thr Lys Asp Asp Thr Val Asn Asp Ala Asn Glu Leu
            420                 425                 430
Gly Lys Gly Asn Pro Phe Ala Met Glu Ile Asn Ile Gln Ala Asn Leu
        435                 440                 445
Trp Arg Asn Phe Leu Tyr Ala Asn Val Ala Leu Tyr Leu Pro Asp Ser
    450                 455                 460
Tyr Lys Tyr Thr Pro Ala Asn Ile Thr Leu Pro Thr Asn Thr Asn Thr
465                 470                 475                 480
Tyr Asp Tyr Met Asn Gly Arg Val Val Ala Pro Ser Leu Val Asp Ala
                485                 490                 495
Tyr Ile Asn Ile Gly Ala Arg Trp Ser Leu Asp Pro Met Asp Asn Val
            500                 505                 510
Asn Pro Phe Asn His His Arg Asn Ala Gly Leu Arg Tyr Arg Ser Met
        515                 520                 525
Leu Leu Gly Asn Gly Arg Tyr Val Pro Phe His Ile Gln Val Pro Gln
    530                 535                 540
Lys Phe Phe Ala Ile Lys Ser Leu Leu Leu Leu Pro Gly Ser Tyr Thr
545                 550                 555                 560
Tyr Glu Trp Asn Phe Arg Lys Asp Val Asn Met Ile Leu Gln Ser Ser
                565                 570                 575
Leu Gly Asn Asp Leu Arg Thr Asp Gly Ala Ser Ile Ala Phe Thr Ser
            580                 585                 590
Ile Asn Leu Tyr Ala Thr Phe Phe Pro Met Ala His Asn Thr Ala Ser
        595                 600                 605
Thr Leu Glu Ala Met Leu Arg Asn Asp Thr Asn Asp Gln Ser Phe Asn
    610                 615                 620
Asp Tyr Leu Ser Ala Ala Asn Met Leu Tyr Pro Ile Pro Ala Asn Ala
625                 630                 635                 640
Thr Asn Val Pro Ile Ser Ile Pro Ser Arg Asn Trp Ala Ala Phe Arg
                645                 650                 655
Gly Trp Ser Phe Thr Arg Leu Lys Thr Arg Glu Thr Pro Ser Leu Gly
            660                 665                 670
Ser Gly Phe Asp Pro Tyr Phe Val Tyr Ser Gly Ser Ile Pro Tyr Leu
        675                 680                 685
Asp Gly Thr Phe Tyr Leu Asn His Thr Phe Lys Lys Val Ser Ile Thr
    690                 695                 700
Phe Asp Ser Ser Val Ser Trp Pro Gly Asn Asp Arg Leu Leu Thr Pro
705                 710                 715                 720
Asn Glu Phe Glu Ile Lys Arg Thr Val Asp Gly Glu Gly Tyr Asn Val
                725                 730                 735
Ala Gln Cys Asn Met Thr Lys Asp Trp Phe Leu Val Gln Met Leu Ala
```

```
            740                 745                 750
His Tyr Asn Ile Gly Tyr Gln Gly Phe Tyr Val Pro Glu Gly Tyr Lys
        755                 760                 765
Asp Arg Met Tyr Ser Phe Phe Arg Asn Phe Gln Pro Met Ser Arg Gln
    770                 775                 780
Val Val Asp Glu Val Asn Tyr Lys Asp Tyr Gln Ala Val Thr Leu Ala
785                 790                 795                 800
Tyr Gln His Asn Asn Ser Gly Phe Val Gly Tyr Leu Ala Pro Thr Met
                805                 810                 815
Arg Gln Gly Gln Pro Tyr Pro Ala Asn Tyr Pro Tyr Pro Leu Ile Gly
            820                 825                 830
Lys Ser Ala Val Ala Ser Val Thr Gln Lys Lys Phe Leu Cys Asp Arg
        835                 840                 845
Val Met Trp Arg Ile Pro Phe Ser Ser Asn Phe Met Ser Met Gly Ala
    850                 855                 860
Leu Thr Asp Leu Gly Gln Asn Met Leu Tyr Ala Asn Ser Ala His Ala
865                 870                 875                 880
Leu Asp Met Asn Phe Glu Val Asp Pro Met Asp Glu Ser Thr Leu Leu
                885                 890                 895
Tyr Val Val Phe Glu Val Phe Asp Val Val Arg Val His Gln Pro His
            900                 905                 910
Arg Gly Val Ile Glu Ala Val Tyr Leu Arg Thr Pro Phe Ser Ala Gly
        915                 920                 925
Asn Ala Thr Thr
    930
```

<210> 122
<211> 960
<212> PRT
<213> Chimpanzee Adenovirus- ChAd 3 Hexon

<400> 122

```
Met Ala Thr Pro Ser Met Met Pro Gln Trp Ser Tyr Met His Ile Ser
 1               5                  10                  15
Gly Gln Asp Ala Ser Glu Tyr Leu Ser Pro Gly Leu Val Gln Phe Ala
            20                  25                  30
Arg Ala Thr Glu Ser Tyr Phe Ser Leu Ser Asn Lys Phe Arg Asn Pro
        35                  40                  45
Thr Val Ala Pro Thr His Asp Val Thr Thr Asp Arg Ser Gln Arg Leu
    50                  55                  60
Thr Leu Arg Phe Ile Pro Val Asp Arg Glu Asp Thr Ala Tyr Ser Tyr
65                  70                  75                  80
Lys Ala Arg Phe Thr Leu Ala Val Gly Asp Asn Arg Val Leu Asp Met
                85                  90                  95
Ala Ser Thr Tyr Phe Asp Ile Arg Gly Val Leu Asp Arg Gly Pro Thr
            100                 105                 110
Phe Lys Pro Tyr Ser Gly Thr Ala Tyr Asn Ser Leu Ala Pro Lys Gly
        115                 120                 125
Ala Pro Asn Ser Cys Glu Trp Glu Gln Glu Glu Thr Gln Ala Val Glu
    130                 135                 140
Glu Ala Ala Glu Glu Glu Glu Glu Asp Ala Asp Gly Gln Ala Glu Glu
145                 150                 155                 160
Glu Gln Ala Ala Thr Lys Lys Thr His Val Tyr Ala Gln Ala Pro Leu
                165                 170                 175
```

```
Ser Gly Glu Lys Ile Ser Lys Asp Gly Leu Gln Ile Gly Thr Asp Ala
            180                 185                 190
Thr Ala Thr Glu Gln Lys Pro Ile Tyr Ala Asp Pro Thr Phe Gln Pro
        195                 200                 205
Glu Pro Gln Ile Gly Glu Ser Gln Trp Asn Glu Ala Asp Ala Thr Val
    210                 215                 220
Ala Gly Gly Arg Val Leu Lys Lys Ser Thr Pro Met Lys Pro Cys Tyr
225                 230                 235                 240
Gly Ser Tyr Ala Arg Pro Thr Asn Ala Asn Gly Gly Gln Gly Val Leu
                245                 250                 255
Thr Ala Asn Ala Gln Gly Gln Leu Glu Ser Gln Val Glu Met Gln Phe
            260                 265                 270
Phe Ser Thr Ser Glu Asn Ala Arg Asn Glu Ala Asn Asn Ile Gln Pro
        275                 280                 285
Lys Leu Val Leu Tyr Ser Glu Asp Val His Met Glu Thr Pro Asp Thr
    290                 295                 300
His Leu Ser Tyr Lys Pro Ala Lys Ser Asp Asp Asn Ser Lys Ile Met
305                 310                 315                 320
Leu Gly Gln Gln Ser Met Pro Asn Arg Pro Asn Tyr Ile Gly Phe Arg
                325                 330                 335
Asp Asn Phe Ile Gly Leu Met Tyr Tyr Asn Ser Thr Gly Asn Met Gly
            340                 345                 350
Val Leu Ala Gly Gln Ala Ser Gln Leu Asn Ala Val Val Asp Leu Gln
        355                 360                 365
Asp Arg Asn Thr Glu Leu Ser Tyr Gln Leu Leu Leu Asp Ser Met Gly
    370                 375                 380
Asp Arg Thr Arg Tyr Phe Ser Met Trp Asn Gln Ala Val Asp Ser Tyr
385                 390                 395                 400
Asp Pro Asp Val Arg Ile Ile Glu Asn His Gly Thr Glu Asp Glu Leu
                405                 410                 415
Pro Asn Tyr Cys Phe Pro Leu Gly Gly Ile Gly Val Thr Asp Thr Tyr
            420                 425                 430
Gln Ala Val Lys Thr Asn Asn Gly Asn Asn Gly Gly Gln Val Thr Trp
        435                 440                 445
Thr Lys Asp Glu Thr Phe Ala Asp Arg Asn Glu Ile Gly Val Gly Asn
    450                 455                 460
Asn Phe Ala Met Glu Ile Asn Leu Ser Ala Asn Leu Trp Arg Asn Phe
465                 470                 475                 480
Leu Tyr Ser Asn Val Ala Leu Tyr Leu Pro Asp Lys Leu Lys Tyr Asn
                485                 490                 495
Pro Ser Asn Val Asp Ile Ser Asp Asn Pro Asn Thr Tyr Asp Tyr Met
            500                 505                 510
Asn Lys Arg Val Val Ala Pro Gly Leu Val Asp Cys Tyr Ile Asn Leu
        515                 520                 525
Gly Ala Arg Trp Ser Leu Asp Tyr Met Asp Asn Val Asn Pro Phe Asn
    530                 535                 540
His His Arg Asn Ala Gly Leu Arg Tyr Arg Ser Met Leu Leu Gly Asn
545                 550                 555                 560
Gly Arg Tyr Val Pro Phe His Ile Gln Val Pro Gln Lys Phe Phe Ala
                565                 570                 575
Ile Lys Asn Leu Leu Leu Leu Pro Gly Ser Tyr Thr Tyr Glu Trp Asn
            580                 585                 590
Phe Arg Lys Asp Val Asn Met Val Leu Gln Ser Ser Leu Gly Asn Asp
        595                 600                 605
Leu Arg Val Asp Gly Ala Ser Ile Lys Phe Glu Ser Ile Cys Leu Tyr
```

```
    610                 615                 620
Ala Thr Phe Phe Pro Met Ala His Asn Thr Ala Ser Thr Leu Glu Ala
625                 630                 635                 640
Met Leu Arg Asn Asp Thr Asn Asp Gln Ser Phe Asn Asp Tyr Leu Ser
                645                 650                 655
Ala Ala Asn Met Leu Tyr Pro Ile Pro Ala Asn Ala Thr Asn Val Pro
            660                 665                 670
Ile Ser Ile Pro Ser Arg Asn Trp Ala Ala Phe Arg Gly Trp Ala Phe
        675                 680                 685
Thr Arg Leu Lys Thr Lys Glu Thr Pro Ser Leu Gly Ser Gly Phe Asp
    690                 695                 700
Pro Tyr Tyr Thr Tyr Ser Gly Ser Ile Pro Tyr Leu Asp Gly Thr Phe
705                 710                 715                 720
Tyr Leu Asn His Thr Phe Lys Lys Val Ser Val Thr Phe Asp Ser Ser
                725                 730                 735
Val Ser Trp Pro Gly Asn Asp Arg Leu Leu Thr Pro Asn Glu Phe Glu
            740                 745                 750
Ile Lys Arg Ser Val Asp Gly Glu Gly Tyr Asn Val Ala Gln Cys Asn
        755                 760                 765
Met Thr Lys Asp Trp Phe Leu Val Gln Met Leu Ala Asn Tyr Asn Ile
    770                 775                 780
Gly Tyr Gln Gly Phe Tyr Ile Pro Glu Ser Tyr Lys Asp Arg Met Tyr
785                 790                 795                 800
Ser Phe Phe Arg Asn Phe Gln Pro Met Ser Arg Gln Val Val Asp Gln
                805                 810                 815
Thr Lys Tyr Lys Asp Tyr Gln Glu Val Gly Ile Ile His Gln His Asn
            820                 825                 830
Asn Ser Gly Phe Val Gly Tyr Leu Ala Pro Thr Met Arg Glu Gly Gln
        835                 840                 845
Ala Tyr Pro Ala Asn Phe Pro Tyr Pro Leu Ile Gly Lys Thr Ala Val
    850                 855                 860
Asp Ser Ile Thr Gln Lys Lys Phe Leu Cys Asp Arg Thr Leu Trp Arg
865                 870                 875                 880
Ile Pro Phe Ser Ser Asn Phe Met Ser Met Gly Ala Leu Ser Asp Leu
                885                 890                 895
Gly Gln Asn Leu Leu Tyr Ala Asn Ser Ala His Ala Leu Asp Met Thr
            900                 905                 910
Phe Glu Val Asp Pro Met Asp Glu Pro Thr Leu Leu Tyr Val Leu Phe
        915                 920                 925
Glu Val Phe Asp Val Val Arg Val His Gln Pro His Arg Gly Val Ile
    930                 935                 940
Glu Thr Val Tyr Leu Arg Thr Pro Phe Ser Ala Gly Asn Ala Thr Thr
945                 950                 955                 960


<210> 123
<211> 937
<212> PRT
<213> Chimpanzee Adenovirus- ChAd 6 Hexon

<400> 123
Met Ala Thr Pro Ser Met Leu Pro Gln Trp Ala Tyr Met His Ile Ala
 1               5                  10                  15
Gly Gln Asp Ala Ser Glu Tyr Leu Ser Pro Gly Leu Val Gln Phe Ala
            20                  25                  30
```

```
Arg Ala Thr Asp Thr Tyr Phe Ser Leu Gly Asn Lys Phe Arg Asn Pro
        35                  40                  45
Thr Val Ala Pro Thr His Asp Val Thr Thr Asp Arg Ser Gln Arg Leu
    50                  55                  60
Thr Leu Arg Phe Val Pro Val Asp Arg Glu Asp Asn Thr Tyr Ser Tyr
65                  70                  75                  80
Lys Val Arg Tyr Thr Leu Ala Val Gly Asp Asn Arg Val Leu Asp Met
                85                  90                  95
Ala Ser Thr Tyr Phe Asp Ile Arg Gly Val Leu Asp Arg Gly Pro Ser
            100                 105                 110
Phe Lys Pro Tyr Ser Gly Thr Ala Tyr Asn Ser Leu Ala Pro Lys Gly
        115                 120                 125
Ala Pro Asn Thr Ser Gln Trp Ile Thr Lys Asp Asn Gly Thr Asp Lys
    130                 135                 140
Thr Tyr Ser Phe Gly Asn Ala Pro Val Arg Gly Leu Asp Ile Thr Glu
145                 150                 155                 160
Glu Gly Leu Gln Ile Gly Pro Asp Glu Ser Gly Gly Glu Ser Lys Lys
                165                 170                 175
Ile Phe Ala Asp Lys Thr Tyr Gln Pro Glu Pro Gln Leu Gly Asp Glu
            180                 185                 190
Glu Trp His Asp Thr Ile Gly Ala Glu Asp Lys Tyr Gly Gly Arg Ala
        195                 200                 205
Leu Lys Pro Ala Thr Asn Met Lys Pro Cys Tyr Gly Ser Phe Ala Lys
    210                 215                 220
Pro Thr Asn Ala Lys Gly Gly Gln Ala Lys Ser Arg Thr Lys Asp Asp
225                 230                 235                 240
Gly Thr Thr Glu Pro Asp Ile Asp Met Ala Phe Phe Asp Asp Arg Ser
                245                 250                 255
Gln Gln Ala Ser Phe Ser Pro Glu Leu Val Leu Tyr Thr Glu Asn Val
            260                 265                 270
Asp Leu Asp Thr Pro Asp Thr His Ile Ile Tyr Lys Pro Gly Thr Asp
        275                 280                 285
Glu Thr Ser Ser Ser Phe Asn Leu Gly Gln Gln Ser Met Pro Asn Arg
    290                 295                 300
Pro Asn Tyr Ile Gly Phe Arg Asp Asn Phe Ile Gly Leu Met Tyr Tyr
305                 310                 315                 320
Asn Ser Thr Gly Asn Met Gly Val Leu Ala Gly Gln Ala Ser Gln Leu
                325                 330                 335
Asn Ala Val Val Asp Leu Gln Asp Arg Asn Thr Glu Leu Ser Tyr Gln
            340                 345                 350
Leu Leu Leu Asp Ser Leu Gly Asp Arg Thr Arg Tyr Phe Ser Met Trp
        355                 360                 365
Asn Gln Ala Val Asp Ser Tyr Asp Pro Asp Val Arg Ile Ile Glu Asn
    370                 375                 380
His Gly Val Glu Asp Glu Leu Pro Asn Tyr Cys Phe Pro Leu Asn Gly
385                 390                 395                 400
Val Gly Phe Thr Asp Thr Phe Gln Gly Ile Lys Val Lys Thr Thr Asn
                405                 410                 415
Asn Gly Thr Ala Asn Ala Thr Glu Trp Glu Ser Asp Thr Ser Val Asn
            420                 425                 430
Asn Ala Asn Glu Ile Ala Lys Gly Asn Pro Phe Ala Met Glu Ile Asn
        435                 440                 445
Ile Gln Ala Asn Leu Trp Arg Asn Phe Leu Tyr Ala Asn Val Ala Leu
    450                 455                 460
Tyr Leu Pro Asp Ser Tyr Lys Tyr Thr Pro Ala Asn Ile Thr Leu Pro
```

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465                 470                 475                 480
Ala Asn Thr Asn Thr Tyr Asp Tyr Met Asn Gly Arg Val Val Ala Pro
                485                 490                 495
Ser Leu Val Asp Ala Tyr Ile Asn Ile Gly Ala Arg Trp Ser Leu Asp
            500                 505                 510
Pro Met Asp Asn Val Asn Pro Phe Asn His His Arg Asn Ala Gly Leu
        515                 520                 525
Arg Tyr Arg Ser Met Leu Leu Gly Asn Gly Arg Tyr Val Pro Phe His
    530                 535                 540
Ile Gln Val Pro Gln Lys Phe Phe Ala Ile Lys Ser Leu Leu Leu Leu
545                 550                 555                 560
Pro Gly Ser Tyr Thr Tyr Glu Trp Asn Phe Arg Lys Asp Val Asn Met
                565                 570                 575
Ile Leu Gln Ser Ser Leu Gly Asn Asp Leu Arg Thr Asp Gly Ala Ser
            580                 585                 590
Ile Ala Phe Thr Ser Ile Asn Leu Tyr Ala Thr Phe Phe Pro Met Ala
        595                 600                 605
His Asn Thr Ala Ser Thr Leu Glu Ala Met Leu Arg Asn Asp Thr Asn
    610                 615                 620
Asp Gln Ser Phe Asn Asp Tyr Leu Ser Ala Ala Asn Met Leu Tyr Pro
625                 630                 635                 640
Ile Pro Ala Asn Ala Thr Asn Val Pro Ile Ser Ile Pro Ser Arg Asn
                645                 650                 655
Trp Ala Ala Phe Arg Gly Trp Ser Phe Thr Arg Leu Lys Thr Arg Glu
            660                 665                 670
Thr Pro Ser Leu Gly Ser Gly Phe Asp Pro Tyr Phe Val Tyr Ser Gly
        675                 680                 685
Ser Ile Pro Tyr Leu Asp Gly Thr Phe Tyr Leu Asn His Thr Phe Lys
    690                 695                 700
Lys Val Ser Ile Thr Phe Asp Ser Ser Val Ser Trp Pro Gly Asn Asp
705                 710                 715                 720
Arg Leu Leu Thr Pro Asn Glu Phe Glu Ile Lys Arg Thr Val Asp Gly
                725                 730                 735
Glu Gly Tyr Asn Val Ala Gln Cys Asn Met Thr Lys Asp Trp Phe Leu
            740                 745                 750
Val Gln Met Leu Ala His Tyr Asn Ile Gly Tyr Gln Gly Phe Tyr Val
        755                 760                 765
Pro Glu Gly Tyr Lys Asp Arg Met Tyr Ser Phe Phe Arg Asn Phe Gln
    770                 775                 780
Pro Met Ser Arg Gln Val Val Asp Glu Val Asn Tyr Lys Asp Tyr Gln
785                 790                 795                 800
Ala Val Thr Leu Ala Tyr Gln His Asn Asn Ser Gly Phe Val Gly Tyr
                805                 810                 815
Leu Ala Pro Thr Met Arg Gln Gly Gln Pro Tyr Pro Ala Asn Tyr Pro
            820                 825                 830
Tyr Pro Leu Ile Gly Lys Ser Ala Val Ala Ser Val Thr Gln Lys Lys
        835                 840                 845
Phe Leu Cys Asp Arg Val Met Trp Arg Ile Pro Phe Ser Ser Asn Phe
    850                 855                 860
Met Ser Met Gly Ala Leu Thr Asp Leu Gly Gln Asn Met Leu Tyr Ala
865                 870                 875                 880
Asn Ser Ala His Ala Leu Asp Met Asn Phe Glu Val Asp Pro Met Asp
                885                 890                 895
Glu Ser Thr Leu Leu Tyr Val Val Phe Glu Val Phe Asp Val Val Arg
            900                 905                 910
```

```
Val His Gln Pro His Arg Gly Val Ile Glu Ala Val Tyr Leu Arg Thr
        915                 920                 925
Pro Phe Ser Ala Gly Asn Ala Thr Thr
    930                 935
```

<210> 124
<211> 956
<212> PRT
<213> Chimpanzee Adenovirus- C1 Hexon

<400> 124

```
Met Ala Thr Pro Ser Met Leu Pro Gln Trp Ala Tyr Met His Ile Ala
 1               5                  10                  15
Gly Gln Asp Ala Ser Glu Tyr Leu Ser Pro Gly Leu Val Gln Phe Ala
            20                  25                  30
Arg Ala Thr Asp Thr Tyr Phe Asn Leu Gly Asn Lys Phe Arg Asn Pro
        35                  40                  45
Thr Val Ala Pro Thr His Asp Val Thr Thr Asp Arg Ser Gln Arg Leu
    50                  55                  60
Met Leu Arg Phe Val Pro Val Asp Arg Glu Asp Asn Thr Tyr Ser Tyr
65                  70                  75                  80
Lys Val Arg Tyr Thr Leu Ala Val Gly Asp Asn Arg Val Leu Asp Met
                85                  90                  95
Ala Ser Thr Phe Phe Asp Ile Arg Gly Val Leu Asp Arg Gly Pro Ser
            100                 105                 110
Phe Lys Pro Tyr Ser Gly Ser Ala Tyr Asn Ser Leu Ala Pro Lys Gly
        115                 120                 125
Ala Pro Asn Thr Ser Gln Trp Leu Asp Lys Gly Val Thr Thr Thr Asp
    130                 135                 140
Asn Asn Thr Glu Asn Gly Asp Glu Glu Asp Glu Val Ala Glu Glu Gly
145                 150                 155                 160
Glu Glu Glu Lys Gln Ala Thr Tyr Thr Phe Gly Asn Ala Pro Val Lys
                165                 170                 175
Ala Glu Ala Glu Ile Thr Lys Glu Gly Leu Pro Ile Gly Leu Glu Val
            180                 185                 190
Pro Ser Glu Gly Asp Pro Lys Pro Ile Tyr Ala Asp Lys Leu Tyr Gln
        195                 200                 205
Pro Glu Pro Gln Val Gly Glu Glu Ser Trp Thr Asp Thr Asp Gly Thr
    210                 215                 220
Asp Glu Lys Tyr Gly Gly Arg Ala Leu Lys Pro Glu Thr Lys Met Lys
225                 230                 235                 240
Pro Cys Tyr Gly Ser Phe Ala Lys Pro Thr Asn Val Lys Gly Gly Gln
                245                 250                 255
Ala Lys Val Lys Lys Val Glu Glu Gly Lys Val Glu Tyr Asp Ile Asp
            260                 265                 270
Met Asn Phe Phe Asp Leu Arg Ser Gln Lys Thr Gly Leu Lys Pro Lys
        275                 280                 285
Ile Val Met Tyr Ala Glu Asn Val Asp Leu Glu Thr Pro Asp Thr His
    290                 295                 300
Val Val Tyr Lys Pro Gly Ala Ser Asp Ala Ser Ser His Ala Asn Leu
305                 310                 315                 320
Gly Gln Gln Ser Met Pro Asn Arg Pro Asn Tyr Ile Gly Phe Arg Asp
                325                 330                 335
Asn Phe Ile Gly Leu Met Tyr Tyr Asn Ser Thr Gly Asn Met Gly Val
```

```
            340                 345                 350
Leu Ala Gly Gln Ala Ser Gln Leu Asn Ala Val Val Asp Leu Gln Asp
        355                 360                 365
Arg Asn Thr Glu Leu Ser Tyr Gln Leu Leu Leu Asp Ser Leu Gly Asp
    370                 375                 380
Arg Thr Arg Tyr Phe Ser Met Trp Asn Gln Ala Val Asp Ser Tyr Asp
385                 390                 395                 400
Pro Asp Val Arg Val Ile Glu Asn His Gly Val Glu Asp Glu Leu Pro
                405                 410                 415
Asn Tyr Cys Phe Pro Leu Asp Gly Val Gly Pro Arg Thr Asp Ser Tyr
            420                 425                 430
Lys Gly Ile Glu Thr Asn Gly Asp Glu Asn Thr Thr Trp Lys Asp Leu
        435                 440                 445
Asp Pro Asn Gly Ile Ser Glu Leu Ala Lys Gly Asn Pro Phe Ala Met
    450                 455                 460
Glu Ile Asn Ile Gln Ala Asn Leu Trp Arg Ser Phe Leu Tyr Ser Asn
465                 470                 475                 480
Val Ala Leu Tyr Leu Pro Asp Ser Tyr Lys Tyr Thr Pro Thr Asn Val
                485                 490                 495
Thr Leu Pro Glu Asn Lys Asn Thr Tyr Asp Tyr Met Asn Gly Arg Val
            500                 505                 510
Val Pro Pro Ser Leu Val Asp Thr Tyr Val Asn Ile Gly Ala Arg Trp
        515                 520                 525
Ser Leu Asp Ala Met Asp Asn Val Asn Pro Phe Asn His His Arg Asn
    530                 535                 540
Ala Gly Leu Arg Tyr Arg Ser Met Leu Leu Gly Asn Gly Arg Tyr Val
545                 550                 555                 560
Pro Phe His Ile Gln Val Pro Gln Lys Phe Phe Ala Val Lys Asn Leu
                565                 570                 575
Leu Leu Leu Pro Gly Ser Tyr Thr Tyr Glu Trp Asn Phe Arg Lys Asp
            580                 585                 590
Val Asn Met Val Leu Gln Ser Ser Leu Gly Asn Asp Leu Arg Val Asp
        595                 600                 605
Gly Ala Ser Ile Ser Phe Thr Ser Ile Asn Leu Tyr Ala Thr Phe Phe
    610                 615                 620
Pro Met Ala His Asn Thr Ala Ser Thr Leu Glu Ala Met Leu Arg Asn
625                 630                 635                 640
Asp Thr Asn Asp Gln Ser Phe Asn Asp Tyr Leu Ser Ala Ala Asn Met
                645                 650                 655
Leu Tyr Pro Ile Pro Ala Asn Ala Thr Asn Val Pro Ile Ser Ile Pro
            660                 665                 670
Ser Arg Asn Trp Ala Ala Phe Arg Gly Trp Ser Phe Thr Arg Leu Lys
        675                 680                 685
Thr Lys Glu Thr Pro Ser Leu Gly Ser Gly Phe Asp Pro Tyr Phe Val
    690                 695                 700
Tyr Ser Gly Ser Ile Pro Tyr Leu Asp Gly Thr Phe Tyr Leu Asn His
705                 710                 715                 720
Thr Phe Lys Lys Val Ser Ile Met Phe Asp Ser Ser Val Ser Trp Pro
                725                 730                 735
Gly Asn Asp Arg Leu Leu Thr Pro Asn Glu Phe Glu Ile Lys Arg Thr
            740                 745                 750
Val Asp Gly Glu Gly Tyr Asn Val Ala Gln Cys Asn Met Thr Lys Asp
        755                 760                 765
Trp Phe Leu Val Gln Met Leu Ala Asn Tyr Asn Ile Gly Tyr Gln Gly
    770                 775                 780
```

```
Phe Tyr Val Pro Glu Gly Tyr Lys Asp Arg Met Tyr Ser Phe Phe Arg
785                 790                 795                 800
Asn Phe Gln Pro Met Ser Arg Gln Val Val Asp Glu Ile Asn Tyr Lys
                805                 810                 815
Asp Tyr Lys Ala Val Ala Val Pro Tyr Gln His Asn Asn Ser Gly Phe
            820                 825                 830
Val Gly Tyr Met Ala Pro Thr Met Arg Gln Gly Gln Ala Tyr Pro Ala
        835                 840                 845
Asn Tyr Pro Tyr Pro Leu Ile Gly Thr Thr Ala Val Thr Ser Val Thr
    850                 855                 860
Gln Lys Lys Phe Leu Cys Asp Arg Thr Met Trp Arg Ile Pro Phe Ser
865                 870                 875                 880
Ser Asn Phe Met Ser Met Gly Ala Leu Thr Asp Leu Gly Gln Asn Leu
                885                 890                 895
Leu Tyr Ala Asn Ser Ala His Ala Leu Asp Met Thr Phe Glu Val Asp
            900                 905                 910
Pro Met Asp Glu Pro Thr Leu Leu Tyr Leu Leu Phe Glu Val Phe Asp
        915                 920                 925
Val Val Arg Val His Gln Pro His Arg Gly Val Ile Glu Ala Val Tyr
    930                 935                 940
Leu Arg Thr Pro Phe Ser Ala Gly Asn Ala Thr Thr
945                 950                 955
```

<210> 125
<211> 933
<212> PRT
<213> Chimpanzee Adenovirus- CV68 Hexon

<400> 125

```
Met Ala Thr Pro Ser Met Leu Pro Gln Trp Ala Tyr Met His Ile Ala
 1               5                  10                  15
Gly Gln Asp Ala Ser Glu Tyr Leu Ser Pro Gly Leu Val Gln Phe Ala
            20                  25                  30
Arg Ala Thr Asp Thr Tyr Phe Ser Leu Gly Asn Lys Phe Arg Asn Pro
        35                  40                  45
Thr Val Ala Pro Thr His Asp Val Thr Thr Asp Arg Ser Gln Arg Leu
    50                  55                  60
Thr Leu Arg Phe Val Pro Val Asp Arg Glu Asp Asn Thr Tyr Ser Tyr
65                  70                  75                  80
Lys Val Arg Tyr Thr Leu Ala Val Gly Asp Asn Arg Val Leu Asp Met
                85                  90                  95
Ala Ser Thr Tyr Phe Asp Ile Arg Gly Val Leu Asp Arg Gly Pro Ser
            100                 105                 110
Phe Lys Pro Tyr Ser Gly Thr Ala Tyr Asn Ser Leu Ala Pro Lys Gly
        115                 120                 125
Ala Pro Asn Thr Cys Gln Trp Thr Tyr Lys Ala Asp Gly Glu Thr Ala
    130                 135                 140
Thr Glu Lys Thr Tyr Thr Tyr Gly Asn Ala Pro Val Gln Gly Ile Asn
145                 150                 155                 160
Ile Thr Lys Asp Gly Ile Gln Leu Gly Thr Asp Thr Asp Asp Gln Pro
                165                 170                 175
Ile Tyr Ala Asp Lys Thr Tyr Gln Pro Glu Pro Gln Val Gly Asp Ala
            180                 185                 190
Glu Trp His Asp Ile Thr Gly Thr Asp Glu Lys Tyr Gly Gly Arg Ala
```

```
        195                 200                 205
Leu Lys Pro Asp Thr Lys Met Lys Pro Cys Tyr Gly Ser Phe Ala Lys
    210                 215                 220
Pro Thr Asn Lys Glu Gly Gly Gln Ala Asn Val Lys Thr Gly Thr Gly
225                 230                 235                 240
Thr Thr Lys Glu Tyr Asp Ile Asp Met Ala Phe Phe Asp Asn Arg Ser
                245                 250                 255
Ala Ala Ala Ala Gly Leu Ala Pro Glu Ile Val Leu Tyr Thr Glu Asn
            260                 265                 270
Val Asp Leu Glu Thr Pro Asp Thr His Ile Val Tyr Lys Ala Gly Thr
        275                 280                 285
Asp Asp Ser Ser Ser Ser Ile Asn Leu Gly Gln Gln Ala Met Pro Asn
    290                 295                 300
Arg Pro Asn Tyr Ile Gly Phe Arg Asp Asn Phe Ile Gly Leu Met Tyr
305                 310                 315                 320
Tyr Asn Ser Thr Gly Asn Met Gly Val Leu Ala Gly Gln Ala Ser Gln
                325                 330                 335
Leu Asn Ala Val Val Asp Leu Gln Asp Arg Asn Thr Glu Leu Ser Tyr
            340                 345                 350
Gln Leu Leu Leu Asp Ser Leu Gly Asp Arg Thr Arg Tyr Phe Ser Met
        355                 360                 365
Trp Asn Gln Ala Val Asp Ser Tyr Asp Pro Asp Val Arg Ile Ile Glu
    370                 375                 380
Asn His Gly Val Glu Asp Glu Leu Pro Asn Tyr Cys Phe Pro Leu Asp
385                 390                 395                 400
Ala Val Gly Arg Thr Asp Thr Tyr Gln Gly Ile Lys Ala Asn Gly Thr
                405                 410                 415
Asp Gln Thr Thr Trp Thr Lys Asp Asp Ser Val Asn Asp Ala Asn Glu
            420                 425                 430
Ile Gly Lys Gly Asn Pro Phe Ala Met Glu Ile Asn Ile Gln Ala Asn
        435                 440                 445
Leu Trp Arg Asn Phe Leu Tyr Ala Asn Val Ala Leu Tyr Leu Pro Asp
    450                 455                 460
Ser Tyr Lys Tyr Thr Pro Ala Asn Val Thr Leu Pro Thr Asn Thr Asn
465                 470                 475                 480
Thr Tyr Asp Tyr Met Asn Gly Arg Val Val Ala Pro Ser Leu Val Asp
                485                 490                 495
Ser Tyr Ile Asn Ile Gly Ala Arg Trp Ser Leu Asp Pro Met Asp Asn
            500                 505                 510
Val Asn Pro Phe Asn His His Arg Asn Ala Gly Leu Arg Tyr Arg Ser
        515                 520                 525
Met Leu Leu Gly Asn Gly Arg Tyr Val Pro Phe His Ile Gln Val Pro
    530                 535                 540
Gln Lys Phe Phe Ala Ile Lys Ser Leu Leu Leu Leu Pro Gly Ser Tyr
545                 550                 555                 560
Thr Tyr Glu Trp Asn Phe Arg Lys Asp Val Asn Met Ile Leu Gln Ser
                565                 570                 575
Ser Leu Gly Asn Asp Leu Arg Thr Asp Gly Ala Ser Ile Ser Phe Thr
            580                 585                 590
Ser Ile Asn Leu Tyr Ala Thr Phe Phe Pro Met Ala His Asn Thr Ala
        595                 600                 605
Ser Thr Leu Glu Ala Met Leu Arg Asn Asp Thr Asn Asp Gln Ser Phe
    610                 615                 620
Asn Asp Tyr Leu Ser Ala Ala Asn Met Leu Tyr Pro Ile Pro Ala Asn
625                 630                 635                 640
```

```
Ala Thr Asn Val Pro Ile Ser Ile Pro Ser Arg Asn Trp Ala Ala Phe
                645                 650                 655
Arg Gly Trp Ser Phe Thr Arg Leu Lys Thr Lys Glu Thr Pro Ser Leu
            660                 665                 670
Gly Ser Gly Phe Asp Pro Tyr Phe Val Tyr Ser Gly Ser Ile Pro Tyr
        675                 680                 685
Leu Asp Gly Thr Phe Tyr Leu Asn His Thr Phe Lys Lys Val Ser Ile
    690                 695                 700
Thr Phe Asp Ser Ser Val Ser Trp Pro Gly Asn Asp Arg Leu Leu Thr
705                 710                 715                 720
Pro Asn Glu Phe Glu Ile Lys Arg Thr Val Asp Gly Glu Gly Tyr Asn
                725                 730                 735
Val Ala Gln Cys Asn Met Thr Lys Asp Trp Phe Leu Val Gln Met Leu
            740                 745                 750
Ala His Tyr Asn Ile Gly Tyr Gln Gly Phe Tyr Val Pro Glu Gly Tyr
        755                 760                 765
Lys Asp Arg Met Tyr Ser Phe Phe Arg Asn Phe Gln Pro Met Ser Arg
    770                 775                 780
Gln Val Val Asp Glu Val Asn Tyr Lys Asp Tyr Gln Ala Val Thr Leu
785                 790                 795                 800
Ala Tyr Gln His Asn Asn Ser Gly Phe Val Gly Tyr Leu Ala Pro Thr
                805                 810                 815
Met Arg Gln Gly Gln Pro Tyr Pro Ala Xaa Tyr Pro Tyr Pro Leu Ile
            820                 825                 830
Gly Lys Ser Ala Val Thr Ser Val Thr Gln Lys Lys Phe Leu Cys Asp
        835                 840                 845
Arg Val Met Trp Arg Ile Pro Phe Ser Ser Asn Phe Met Ser Met Gly
    850                 855                 860
Ala Leu Thr Asp Leu Gly Gln Asn Met Leu Tyr Ala Asn Ser Ala His
865                 870                 875                 880
Ala Leu Asp Met Asn Phe Glu Val Asp Pro Met Asp Glu Ser Thr Leu
                885                 890                 895
Leu Tyr Val Val Phe Glu Val Phe Asp Val Val Arg Val His Gln Pro
            900                 905                 910
His Arg Gly Val Ile Glu Ala Val Tyr Xaa Arg Thr Pro Phe Ser Ala
        915                 920                 925
Gly Asn Ala Thr Thr
    930
```